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October 25, 2001, 11:25:36 ; Search time 82.56 Seconds (without alignments) 8921.131 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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e greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.		Description	COC T # LOGIL dayeM	Wheat IEC1 # 3 ood	Sovbean TRC1 # 2 C	Southean Incl. # 2 C	Southean 1 FC1 # 3 C	Arabidonsis lestin	3 4 kh Betut fragm	Arabidoneis lost:	7 4 kh Bond frage	Arabidonsis leaf	CDNA sequence of a	•
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ater t} rived b	æ	Query	100.0	19.3	17.1	16.7	16.4	15.3	15.3	15.3	15.3	15.1	15.1	
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212212	222222222222222222222222222222222222222	20 13 13 13 13 13 13 16 16 16 18 20 20
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	4.0.00 4.0.00 9.0.00 9.0.00 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.000 9.0.0000 9.0.000 9.0.000 9.0.000 9.0000	
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12 13 14 15 17	18 22 23 24 25 27 26 30 31 31 32	0 33333 4444 440 60 644 643 643 643 643 643 643 643 643 643

## ALIGNMENTS

AAA27450 standard; cDNA; 1173 BP.

RESULT AAA27450

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Maize; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss.
                                                                                                                                                                                                                                                                                  Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
                                                                                                                                               /product= "Maize LEC1"
                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                  Location/Qualifiers
69..905
/*tag= a
                                              Maize LEC1 # 1 coding sequence.
                                                                                                                                                                                                                           98US-0107643.
98US-0107810.
                                                                                                                                                                                                        99WO-US26514.
                            11-SEP-2000 (first entry)
                                                                                                                                                                  WO200028058-A2.
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10-NOV-1998;
                                                                                                                                                                                    18-MAY-2000
          AAA27450;
                                                                                                Zea mays.
                                                                                                                  Key
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a

transcriptional activator. LECL. This sequence encodes a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction of sexual reproduction because the integement, or each specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 curansgenic high positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of present sequence is the coding sequence of maize leafy cotyledon 1 New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -Claim 1; Page 76-77; 94pp; English. WPI; 2000-376568/32. regenerated plants. P-PSDB; AAY96214. 

Sequence 1173 BP; 225 A; 392 C; 366 G; 190 T; 0 other;

ö acgacatgcagatgcacgccatgtacgggggaacggccgtgccccgccggcggggc 660 aggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgc 240 181 aggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgtgctgccggcgc 240 360 480 480 540 540 61 gagagecaatggactccagcagetteeteetgeegeeggeggggagaatggeteggegg 120 121 cgggcggcgacaacaatggcgcgctgctcagcagcatgcggcggcggcgatccgcgagc 180 121 cgggcggcgacaacaatggcggcgctgctcagcagcatgcggcggcggcgatccgcgagc 180 gagagecaatggactecageagettectecetgeegeeggeggagaatggeteggegg 120 0; Gaps 301 getteateacggggggaggecaacgageggtgeeagcgggageageagaecateaceg gegectacetecacegetacegegagttegagggegaegegegegegtegggetegtee cgggggccgcccatcgcgcggcggcgaccaccacccgcactccatgtcgccagcggcga gegectaectecaecgetaeegegagttegagggegaegegegegegteggetegtee 100.0%; Score 1173; DB 21; Length 1173; 100.0%; Pred. No. 5.5e-210; tive 0; Mismatches 0; Indels 0; Matches 1173; Conservative Best Local Similarity Query Match 361 421 481 541 301 481 601 61 181 361 421 9 δ g ò g ŏ g ò QQ ö g δ g ò a ò ŏ à ò

1081 gcagtcgtagaagtgttcaatgcttgccagtgtgttgttttagggccggggtaaaccatc 1140 961 cgctgtattgtacacgcatgcacgtacgtatcggcggctagctctcctgtttaagttgta 1020 1081 gcagtcgtagaagtgttcaatgcttgccagtgtgttgttttagggccggggtaaaccatc 1140 961 cgctgtattgtacacgcatgcacgtacgtatcggcggctagctctcctgtttaagttgta 1020 840 721 acgegtacgageceaegtacggeggtgageaegecatggetgeatactatggaggegeeg 780 900 900 cgtacgcgcccggcaacggcgggagcggcggcagtggcagtggcggcggtggtgg 781 cgtacgcgcccggcaacggcgggagcggcgacggcagtggcagtggcggcggtggcgggga 721 acgcgtacgagcccacgtacggcggtgagcacgccatggctgcatactatggaggcgccg 1141 cgatgagattatttcaaaaaaaaaaaaaaaaa 1173 661 781 g g QQ δ g à ð g δ g ò qq δŽ qq ò g ð δ

Wheat; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss. Location/Qualifiers AAA27462 standard; cDNA; 1098 BP. Wheat LEC1 # 3 coding sequence. 11-SEP-2000 (first entry) Ø 55..897 Triticum aestivum. AAA27462; Key AAA27462 

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RESULT

/product= "Wheat LEC1" 98US-0107643. 98US-0107810. 99WO-US26514 /\*tag= WO200028058-A2 09-NOV-1998; 10-NOV-1998; 18-MAY-2000

Cahoon RE; M, Rasco-Gaunt S, Nadimpalli R; Klein TM, Gregory CA, (PION-) PIONEER HI-BRED INT INC (DUPO ) DU PONT DE NEMOURS & CO Gordon-Kamm WJ, Hoerster GJ, Lowe KS, Sun X,

DE NEMOURS & CO E I.

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WPI; 2000-376568/32.
  P-PSDB; AAY96222
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particularly Leafy cotyledon l'transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell New HAP3-type CCAAT-box binding transcriptional activators, particularly

Claim 1; Page 91-93; 94pp; English.

The present sequence is the coding sequence of wheat leafy cotyledon I transcriptional activator, LEC1. This sequence encodes a RAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by assexual reproduction, LEC1 expression in the nuclellus integument, or eall specific expression in the megaspore mother cell would trigger production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In edition, LEC1 could be used for increasing transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.

Sequence 1098 BP; 214 A; 336 C; 357 G; 191 T; 0 other;

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                                                                  catgoggoggoggatcogcgagcaggaccggctgatgccgatcgcgaacgtgatcogc 215
                                                                                                                                                      103 caggggacgccggtggtgcgggagcaggaccggctgatgccgatcgcgaacgtgatccgc 162
                                                                                                                                    276 caggagtgcgtgtcggagtacatcagcttcatcacgggggaggccaacgagcggtgccag 335
                                                                                                                                                                                                                         336 cgggagcagcaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggc 395
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                                           0; Gaps
19.3%; Score 226.4; DB 21; Length 1098; 67.7%; Pred. No. 6.6e-34; tive 0; Mismatches 151; Indels 0;
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Soybean LEC1 # 2 coding sequence.
       AAA27460 standard; cDNA; 1121 BP.
                                                    11-SEP-2000 (first entry)
AAA27460
                              SXEXE
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Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss. /transl\_except= (pos:1059..1064.aa:Asn)
/transl\_except= (pos:1055..1100.aa:Cys)
/transl\_except= (pos:1103..1106.aa:Phe)
/note= "Codons have apparent insertions of three nucleotides which encode stop codons" (pos:741..746,aa:Gln) (pos:765..770,aa:Cys) (pos:783..788,aa:Leu) (pos:822..827,aa:Ser) (pos:828..833,aa:Ser) (pos:930..935,aa:Tyr) (pos:999..1007,aa:Trp) (pos:1008..1016,aa:Trp) (pos:1059..1064,aa:Asn) (pos:945..950,aa:Ala) (pos:999..1007,aa:Trp /transl\_except= (pos:672..677,aa:11e) /transl\_except= (pos:678..686,aa:Asn) 731,aa:Asp) Location/Qualifiers 3..1121 /product= "Soybean /transl\_except= Ø /partial /\*tag= Glycine max

WO200028058-A2. 18-MAY-2000. 99WO-US26514.

98US-0107810. 98US-0107643 10-NOV-1998;

(DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC

Rasco-Gaunt S, Cahoon RE; Gregory CA, Nadimpalli R; Gordon-Kamm WJ, Klein TM, Hoerster GJ, Lowe KS, Sun X,

P-PSDB; AAY96220, AAY96224. WPI; 2000-376568/32

New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -

Claim 1; Page 87-89; 94pp; English.

The present sequence is the coding sequence of soybean leafy cotyledon I transcriptional activator, LEC1. This sequence encodes a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by assexual reproduction, LEC1 expression in the nuclellus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed in addition, LEC1 could be used for increasing transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of

Sequence 1121 BP; 324 A; 233 C; 263 G; 301 T; 0 other;

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0; · Gaps
    Score 200; DB 21; Length 1121;
Pred. No. 5.4e-29;
                                Indels
                                80;
                             0; Mismatches
  17.18;
75.68;
              Best Local Similarity 75.6
Matches 248; Conservative
Query Match
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us-09-435-054-1.rng

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The present sequence is the coding sequence of soybean leafy cotyledon 1 transcriptional activator, LEC1. This sequence encodes a HAP3-type
                                                                                                                311 cgggggaggccaacgagcgttgccagagggagcagcgcaagaccataaccgcagaggacgt 370
                                                                                                                                                                                                   getgtgggccatgagccgcctcggcttcgacgactacgtcgagccgctcggcgcctacct 430
                                                                                                                                                                                                                Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss.
                       131 cagcaaccacagtgcagcaggagagagagaacgaatgcacggtgagggagcaagacaggtt 190
                                                                       131 caacaatggcggcgctgctcagcagcatgcggcgccggcgatccgcgagcaggaccggct 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -
                                                gatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgcacgccaagat
                                                                                                 ctcggacgaccaaggagacgatccaggagtgcgtgtcggagtacatcagcttcatcac
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Nadimpalli R;
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Hoerster GJ, Greg
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P-PSDB; AAY96221.
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CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by assexual reproduction. LEC1 expression in the nuclellus integament, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent Using LEC1 transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gacaactacgeteaceetetetetetttacetteacegetacegegagagtgaaggaga 306
                                                                                                                                                                                                                                                                                                       159 geggegeeggeteegegageaggaceggetegategegaacgtgateegeate 218
                                                                                                                                                                                                                                                                                                                                                                    gagtgcgtgtcggagtacatcagcttcatcacgggggaggccaacgagcggtgccagcgg 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagcagcaaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttc 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gacgactacgtcgagccgctcggcgctccaccgctaccgcgagttcgagggcgac 458
                                                                                                                                                                                                                                                                                                                                                                                                    67 atgogtoggattotgccagcgcacgcgaagatotcagacgacgcgaaggagacgatccag 126
                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                      7 gcaatggcgggagtgagggaacaggaccagtacatgccgatagcgaacgtgataaggatc
                                                                                                                                                                                                                                            DB 21; Length 796;
                                                                                                                                                                                                                                            16.7%; Score 195.8; DB 21; Length
75.9%; Pred. No. 3.2e-28;
Live 0; Mismatches 77; Indels
                                                                                                                                                                                               Sequence 796 BP; 208 A; 174 C; 188 G; 226 T; 0 other;,
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/product= "soybean LEC1 # 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA27456 standard; cDNA; 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 cctgcttctgtcagacgcg 325
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98US-0107810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459 gcgcgcggcgtcgggctcg 477
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                                                                                                                                                                                                                                                               Best Local Similarity 75.9
Matches 242; Conservative
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                                                                                                                                                                   regenerated plants.
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10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA27456;
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399
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promoter

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The present sequence is the coding sequence of soybean leafy octyledon 1 transcriptional activator, LEC1. This sequence encodes a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by sexual reproduction by cell specific expression in the nuclellus integument, or embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of
                                                                                                                                                                                                                         particularly Leafy cotyledon I transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell
                                                                                      Cahoon RE;
                                                                                                                                                                                                        New HAP3-type CCAAT-box binding transcriptional activators,
                                                                                    WJ, Klein TM, Rasco-Gaunt S,
Gregory CA, Nadimpalli R;
                 (PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                 Gordon-Kamm WJ, Klein TM,
                                                                                                                                                                                                                                                                                      Claim 1; Page 80-81; 94pp; English.
                                                                                                   Sun X, Hoerster GJ,
                                                                                                                                            2000-376568/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regenerated plants.
                                                                                                                                                                 P-PSDB; AAY96216
                                                                               Lowe KS,
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Sequence 942 BP; 280 A; 234 C; 212 G; 216 T; 0 other;

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                                                    169 cgatccgcgagcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcg 228
                                                                                                      187 cggtgaggaggaggacaggttcatgccaatcgccaacgtgattaggatcatgcgcaaga 246
                                                                                                                                                                           agaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacg 408
                               0; Gaps
                                                                                                                                                             Score 192.4; DB 21; Length 942;
Pred. No. 1.4e-27;
0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                   tcgagccgctcggcgcctacctccaccgctaccgcgagttcgagggcgac 458
|||| ||| | | | ||||||||||||||| | | |||| ||| |||
tcgaaccgttgaccatgtaccttcaccgctaccgtgaacttgagggtgac 476
  16.4%;
79.0%;
Query Match . 16.49
Best Local Similarity 79.09
Matches 229; Conservative
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LEC1; leafy-cotyledon 1; embryo; transgenic plant; ss.
                                                                                      Arabidopsis leafy-cotyledon 1 (LEC1) gene fragment.
                                                                                                                                   Arabidopsis thaliana ecotype Wassilewskija.
                                                                                                                                                          Location/Qualifiers
                  AAV61023 standard; DNA; 3395 BP
                                                               11-JAN-1999 (first entry)
                                          AAV61023;
                                                                                                                                                          Key
          AAV61023
RESULT
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2217 cggtgaagccaacgagcgttgccaacgtgagcaacgtaagaccataactgctgaagatat 2276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2097 catgccaatcgcaaacgtcataagaatcatgcgtaaaaccttaccgtctcacgccaaaat 2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2157 ctctgacgacgccaaagaaacgattcaagaatgtgtctccgagtacatcagcttcgtgac 2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 ggactccagcagcttcctcctgccgccggcgggagaatggctcggcggcgggggggcgc 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 gggggaggccaacgagcggtgccagcgggagcagcgcaagaccatcaccgccgaggacgt 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 gctgtgggccatgagccgcctcggcttcgacgactacgtcgagccgctcggcgcctacct 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 caacaatggcggcgctgctcagcagcatgcggcggcggcgatccgcgagcaggaccggct 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctcggacgacgccaaggagacgatccaggagtgcgtgtcggagtacatcagcttcatcac 310
                                                                                                                                                                                                                                                                                                                                                                                    New isolated plant leafy cotyledon-1 gene - used to develop products for, e.g. increasing storage protein content in plant tissues, or producing fruit with small and non-viable seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of a 3.4 kb fragment of a Arabidopsis leafy cotyledon-1 (LEC1) gene. The 3.4 kb fragment is able to complement learnest. The LEC1 gene is embryo-specific and is sufficient to induce embryonic pathways in transgenic plants. It encodes a 208-amino acid protein (see AAW71722). LEC1 polynucleotide sequences can be used to modulate development (claimed) of embryos or other organs in plants. Inhibiting expression can be useful e.g. in weed control (by transferring an inhibitory sequence to a weedy species and allowing it to be transmitted through sexual crosses) or to produce fruit with small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and non-viable seed. Enhanced expression of LEC1 polynucleotide sequences can be used to increase storage protein content in plant tissues to improve nutritional value. Promoter sequences of the LEC1 gene can be used to direct expression of desired heterologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3395 BP; 1041 A; 614 C; 542 G; 1197 T; 1 other;
                                                                                                                                                                                                                                                                                                Ohto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes in an embryo-specific or seed-specific manner.
                                                                                                                                                                                                                                                                                            Fischer RL, Goldberg RB, Harada JJ, Lotan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 32-34; 55pp; English.
                                                                                                                                                                                                   98US-0804534.
                                                                                                                                                                 98WO-US02998
                 /*tag= a
1999..2625
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Matches 257; Conservative
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P-PSDB; AAW71722.
                                                                                                                                                               20-FEB-1998;
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The present sequence represents a 3.4 kb Bstyl fragment of Arabidopsis genomic DNA containing sequences from 1.992 kb upstream of the downstream forcyledon 1 (LECI) gene open reading frame to a region 579 bp downstream from the polyA site. The sequence contains the LECI promoter. LECI genes are thought to play a central role in late embryogenesis, in specifying cotyledon identity during embryo development. LECI polypeptides may act as transcription factors. LECI polynucleotides are useful for modulating seed development and for inducing ecotopic development of embryonic tissue in a plant. In both cases, the LECI polynucleotide is introduced into the plant through a sexual cross and is co-expressed in an antisense orientation with a second heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is co-expressed in an antisense orientation with a second heterologous polynucleotide selected from AP2 and RAP2 genes of Arabidopsis. The LEC1 polynucleotide is also useful for targeting expression in a seed, and for preparing expression cassettes for suppressing or enhancing endogenous LEC1 gene expression, which is useful in weed control or for improving nutritional value of plant tissue respectively. LEC1 polypeptides and polynucleotides are especially used for increasing or decreasing storage protein content in cotyledons or leaves. LEC1 also increases reproductive tissue mass, e.g., increases fruit size, seed
2277 cctttgggctatgagcaagcttgggttcgataactacgtggacccctcaccgtgttcat 2336
                                                                                                                                                                                                                                                                                                                                                      Leafy cotyledon 1 gene; LEC1 gene; embryogenesis; cotyledon identity; embryo development; transcription factor; seed development; ecotopic development; embryonic plant tissue; weed control; nutritional value; storage protein; cotyledon; seed; promoter;
                                                                                                                                                                                                                                                                                                               3.4 kb Bstyl fragment of Arabidopsis genomic DNA with LEC1 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note "this is specifically claimed in claim 18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldberg RB, Fischer RL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        reproductive tissue mass; fruit size; seed mass; ss.
                                                                                2337 taaccggtaccgtgagatagagaccga 2363
                                         431 ccaccgctaccgcgagttcgagggcga 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 54-57; 69pp; English.
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                                                                                                                                                                                     AAZ45839 standard; DNA; 3395 BP.
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                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                        25-APR-2000
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                                                                                                                                                                                                                               AAZ45839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                AAZ45839
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                                                                                                                                                 RESULT
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2037 gaacaatggtatcgtggtccagcagcaaccaccatgtgggctcgtgagcaagaccaata 2096
                                                                                                                                                                                                                                   1977 gcacagcaacaacccaaccccaatgaccagctcagtcatagtagccggcggtgacaa 2036
                                                                                                                                                                                          2097 catgocaatogoaaacgtcataagaatcatgogtaaaaccttaccgtctcacgccaaaat 2156
                                                                                                                                                                                                                                                                                                                                                        2277 cctttgggctatgagcaagcttgggttcgataactacgtggacccctcaccgtgttcat 2336
                                                                                                                                                                                                                                                                                                                             gctgtgggccatgagcctcggcttcgacgactacgtcgagcgctcggcgctctacct 430
                                                       ggactccagcagcttcctccctgccgccggcggagaatggctcggcggcggcggcgc 130
                                                                                                           caacaatggcggcgctgctcagcagcatgcggcgccggcgatccgcgagcaggaccggct 190
                                                                                                                                                                ctcggacgacgacgagacgatccaggagtgcgtgtcggagtacatcagcttcatcac 310
                                                                                                                                                                                                                                                                         311 gggggaggccaacgagcggtgccagcgggagcagcgcaagaccatcaccgccgaggacgt 370
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                             Gaps
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Length 3395;
                             0; Mismatches 130; Indels
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Score 179; DB 21;
Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harada JJ, Lotan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana ecotype Wassilewskija.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis leafy-cotyledon 1 (LEC1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                              2337 taaccggtaccgtgagatagagaccga 2363
                                                                                                                                                                                                                                                                                                                                                                                   431 ccaccgctaccgcgagttcgagggcga 457
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4428..5054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV61024 standard; DNA; 7560 BP
 15.3%;
66.4%;
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 Query Match
Best Local Similarity 66.4
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
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This is the nucleotide sequence of a 7.4 kb DNA genomic fragment dentified as carrying the Arabidopsis leafy cotyledon 1 (LEC1) gene. It was isolated from a wild-type genomic library. A 3.4 kb ragment (see AAV61023) of the 7.4 kb DNA is able to complement an lect mutant by transformation. The LEC1 gene is embryo-specific and is sufficient to induce embryonic pathways in transgenic plants. It encodes a 108-amino acid protein (see AAW71722). LEC1 polynuclectide sequences can be used to modulate development (claimed) of embryos or other organs in plants. Inhibiting expression can be useful e.g. in weed control (by transferring an inhibitory sequence.to a weedy species and allowing it to be transmitted through sexual crosses) or to produce fruit with small and non-viable seed. Enhanced expression of LEC1 polynucleotide sequences can be used to increase storage protein content in plant tissues to improve nutritional value. Promoter sequences of the LEC1 gene can be used to direct expression of desired heterologous content in an embryo-specific or seed-specific manner.
             8388888888888888888888888888888888888
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Sequence 7560 BP; 2379 A; 1326 C; 1264 G; 2571 T; 20 other;

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                                                                                                                       4406 gcacagcaacaacccaacccaatgaccagctcagtcatagtagccggcgccggtgacaa 4465
                                                                                                                                                                                                                                                                               4586 ctctgacgacgccaaagaaacgattcaagaatgtgtctccgagtacatcagcttcgtgac 4645
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4646 cggtgaagccaacgagcgttgccaacgtgagcaacgtaagaccataactgctgaagatat 4705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4706 cctttgggctatgagcaagcttgggttcgataactacgtggaccccctcaccgtgttcat 4765
                                                                                131 caacaatggcggcgctgctcagcagcatgcggcggcggcgatccgcgggaccggct 190
                                                                                                                                                                                                                                                                                                                                 251 ctcggacgacgacaaggagacgatccaggagtgcgtgtcggagtacatcactcatcac 310
                                                 0; Gaps
                                                                                                                                                                                                         4466 gaacaatggtatcgtggtccagcagcaaccaccatgtgtggctcgtgagcaagaccaata
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                                                                                                                                                                                                                                                     gatgccgatcgcaacgtgatccgcatcatgcggcgcgtgctgccggcgcacgccaagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 gctgtgggccatgagccgcctcggcttcgacgactacgtcgagccgctcgggcgcctacct
    Length 7560;
                                           0; Mismatches 130; Indels
/ Match .15.3%; Score 179; DB 19;
Local Similarity . 66.4%; Pred. No. 4.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 ccaccgctaccgcgagttcgagggcga 457
                                         Matches 257; Conservative
    Query Match
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Leafy cotyledon 1 gene; LEC1 gene; embryogenesis; cotyledon identity; embryo development; transcription factor; seed development; ecotopic development; embryonic plant tissue; weed control; nutritional value; storage protein; cotyledon; seed; promoter;
                                                                                                                                                                                       7.4 kb EcpRI fragment of Arabidopsis genomic DNA with LEC1 promoter.
                                                                                                                                                                                                                                                                                             reproductive tissue mass; fruit size; seed mass; ss.
 4766 taaccggtaccgtgagatagagaccga 4792
                                                                                     AAZ45840 standard; DNA; 7560 BP
                                                                                                                                                       25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                       AAZ45840;
                                                                   AAZ45840
                                                   RESULT
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W09967405-A2

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The present sequence represents a 7.4 kb EcoRI fragment of Arabidopsis genomic DNA containing the Leafy Cotyledon 1 (LEC1) gene promoter.

LEC1 genes are thought to play a central role in late embryogenesis, in specifying cotyledon identity during embryo development. LEC1 polypeptides may act as transcription factors. LEC1 polynucleotides are useful for modulating seed development and for inducing ecocopic development of embryonic tissue in a plant. In both cases, the LEC1 polynucleotide is introduced into the plant through a sexual cross and is co-expressed in an antisense orientation with a second heterologous polynucleotide selected from AP2 and RAP2 genes of Arabidopsis. The LEC1 polynucleotide is also useful for targeting expression in a seed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and for preparing expression cassettes for suppressing or enhancing endogenous LEC1 gene expression, which is useful in weed control or for improving nutritional value of plant tissue respectively. LEC1 polypeptides and polynucleotides are especially used for increasing or decreasing storage protein content in cotyledons or leaves. LEC1 also increases reproductive tissue mass, e.g., increases fruit size, seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4406 gcacagcaacaacccaaccccaatgaccagctcagtcatagtagccggcggcggtgacaa 4465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 gatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgcacgccaagat 250,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcggacgacgacaaggagacgatccaggagtgcgtgtcggagtacatcagcttcatcac 310
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                                                                                                                                                                                                                                                                                         New embryo-specific gene useful for producing transgenic plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 179; DB 21; Length 75
Pred. No. 4.7e-25;
0; Mismatches 130; Indels
                                                                                                                                                                                                            Goldberg RB, Fischer RL;
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                                                                                                                                                                                                                                                                                                                                 Claim 19; Page 57-64; 69pp; English.
                                                                                                                                                                                                            Ohto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mass, its protein or its oil.
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                                                             99WO-US14384.
                                                                                                  98US-0103478
98US-0193931
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                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                            Harada JJ, Lotan T,
                                                                                                                                                                                                                                                 WPI; 2000-160588/14.
                                                             24 - JUN - 1999;
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17-NOV-1998;
                   29-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LECI) CDNA that engodes a 208-amino acid polypebtide (see AAW71722). The LECI gene clee also AAV61023-24) is embryo-specific and is sufficient to induce embryonic pathways in transgenic plants.

LECI cDNA was isolated from silique-specific cDNA libraries by PCR amplification (see AAV61027-28). LECI polynucleotide sequences can be used to modulate development (claimed) of embryos or other organs in plants. Inhibiting expression can be useful e.g. in weed control (by transferring an inhibitory sequence to a weedy species and allowing it to be transmitted through sexual crosses) or to produce fruit with small and non-viable seed. Enhanced expression of LECI polynucleotide sequences can be used to increase storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaccaccatgtgtggctcgtgagcaagaccaatacatgccaatcgcaaacgtcataagaa 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated plant leafy cotyledon-1 gene - used to develop products for, e.g. increasing storage protein content in plant tissues, or producing fruit with small and non-viable seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein content in plant tissues to improve nutritional value. Promoter sequences of the LEC1 gene can be used to direct expression of desired heterologous genes in an embryo-specific or seed-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccagctcagtcatagtagccggcgccggtgacaagaacaatggtatcgtggtccagcagc 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequence comprises Arabidopsis leafy cotyledon-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohto M;
                                                                                                                                                                   LEC1; leafy-cotyledon 1; embryo; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 627 BP; 162 A; 153 C; 163 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Harada JJ, Lotan T,
                                                                                                                                                                                                      Arabidopsis thaliana ecotype Wassilewskija.
                                                                                                                            Arabidopsis leafy-cotyledon 1 (LEC1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 30; 55pp; English.
               AAV61022 standard; cDNA; 627 BP
                                                                                                                                                                                                                                                                                                                     98WO-US02998
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                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldberg RB,
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                                                                                         11-JAN-1999
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                                                                                                                                                                                                                                                                              27-AUG-1998
                                                    AAV61022;
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AAV61022
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The present sequence encodes a Leafy Cotyledon 1 (LEC1) polypeptide.

LEC1 genes are thought to play a central role in late embryogenesis, in specifying octyledon identity during embryo development. LEC1

Dolypeptides may act as transcription factors. LEC1 polynucleotides are polypeptides may act as transcription factors. LEC1 polynucleotides are development of embryonic tissue in a plant. In both cases, the LEC1

development of embryonic tissue in a plant through a sexual cross and is co-expressed in an antisense orientation with a second heterologous polynucleotide selected from AP2 and RAP2 genes of Arabidopsis. The LEC1 polynucleotide is also useful for targeting expression in a seed, and for preparing expression cassettes for suppressing or enhancing endogenous LEC1 gene expression, which is useful in weed control or for improving nutritional value of plant tissue respectively. LEC1 polypeptides and polynucleotides are especially used for increasing or
                                                                                                                                                                                                                                Leafy cotyledon 1 gene; LEC1 gene; embryogenesis; cotyledon identity;
                                                                                                                                                                   245 gigagcaacgiaagaccaiaacigcigaagaiaticciiigggciaigagcaagciigggi 304
                                                                                                      gggagcagcaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryo development; transcription factor; seed development; ecotopic development; embryonic plant tissue; weed control; nutritional value; storage protein; cotyledon; seed; reproductive tissue mass; fruit size; seed mass; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence of an Arabidopsis leafy cotyledon 1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product- "LEC1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ45838 standard; cDNA; 627 BP.
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                     457 a 457
                                                                                                                                                                                                                                                                                                                                                                                                                                     365 a 365
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Sun X, Hoerster GJ,

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decreasing storage protein content in cotyledons or leaves. LEC1 also increases reproductive tissue mass, e.g., increases fruit size, seed
                                                                                                                                         ccggcgcggagaatggctcggcggcggcggcgacaacaatggcggcgctgctcagcagc 156
                                                                                                                                                                                         157 atgoggoggoggatccgcgagcaggaccggctgatgccgatcgcgaacgtgatccgca 216
                                                                                                                                                                                                                                          tcatgcggcgcgtgctgccggcgcacgccaagatctcggacgacgacgaggaggacgatcc 276
                                                                                                                                                                                                                                                                                          gggagcagcgcaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggct 396
                                                                                                                                                                                                                                                                                                                                                                                              65 aaccaccatgtgtggctcgtgagcaagaccaatacatgccaatcgcaaacgtcataagaa 124
                                                                                                                                                                                                                                                                                                                    185 aagaatgtgtctccgagtacatcagcttcgtgaccggtgaagccaacgagcgttgccaac 244
                                                                                                                                                                                                                                                                                                                                                                     245 gigagcaacgtaagaccataacigcigaagataicciligggciaigagcaagcilgggt 304
                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                      Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss.
                                                                                     15.1%; Score 177; DB 21; Length 627; 68.1%; Pred. No. 9.9e-25; 1ve 0; Mismatches 115; Indels (
                                                Sequence 627 BP; 162 A; 153 C; 163 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Veronia mespilifolia LEC1 coding sequence.
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58..702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA27457 standard; cDNA; 905 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "LEC1"
                         mass, its protein or its oil.
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                                                                                                              Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Veronia mespilifolia.
                                                                                                     Best Local Similarity
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                                                                                        Query Match
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The present sequence is the Veronia mespilifolia coding sequence of leafy cotyledon 1 transcriptional activator, LEC1. This sequence encodes a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of
                                                                                                                                                                                                                                                                              transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the nuclellus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 tecgegageaggaceggetgatgeegategegaaegtgateegeateatgeggegegtge 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 ttcgagaacaggaccgcttcatgccgatagcaaacgtgatccgcatcatgcggaagatcc 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 ttcctccacatgccaagatctctgatgatgccaaagagacgatccaagaatgtgtttcag 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 agtacattagctttgtcacaggcgaggcaaatgaccgctgccagcgtgagcaaaggaaga 376
                                                                                         New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 tgccggcgcacgccaagatctcggacgccaaggagacgacgatcaggagtgcgtgtcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 ccatcacagctgaagatgtgctctgggctatgagcaaactgggatttgatgattatatcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 ccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacgtcg
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Pred. No. 2.4e-24;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 905 BP; 243 A; 184 C; 231 G; 247 T; 0 other;
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/transl_except= (pos:234..236,aa:Xaa)
Gregory CA, Nadimpalli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                     Claim 1; Page 82-83; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize LEC1 # 3 coding sequence.
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Best Local Similarity 74.6%;
Matches 220; Conservative
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                                 WPI; 2000-376568/32
                                                       P-PSDB; AAY96217
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The present sequence is the coding sequence of maize leafy cotyledon 1 transcriptional activator, LEC1. This sequence encodes a hAB3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of saxual reproduction by assaular reproduction, LEC1 expression in the nucleilus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rasco-Gaunt S, Cahoon RE;
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                                                                                                   .458, aa: Xaa)
.464, aa: Xaa)
.470, aa: Xaa)
                                                                                                                                                                                                                                                                                                 581, aa: Xaa)
                                                                                                                                                                                                                                                                                                                       587, aa: Xaa)
                                                                                                                                                                                     488, aa: Xaa)
                                                                                                                                                                                                                    509, aa: Xaa)
                                                                                                                                                                                                                                           542, aa: Xaa)
                                                                                                                                                                                                                                                                       554, aa: Xaa)
                                                                                                                                                                                                                                                                                                                                                       (pos:594..596, aa:Xaa)
                                                   278, aa: Xaa)
                                                                               122,aa:Xaa)
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/note= "Xaa=unknown: no stop codon"
                            , aa :
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berster GJ, Gregory CA, Nadimpalli
                                                                                                                                                                                                                 (pos:507...
                                                                                                                            (pos:462.
(pos:468.
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(pos:507.
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P-PSDB; AAY96219.
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                                                                160 eggegeeggegateegegageaggaeeggetgatgeegategegaaegtgateegeatea 219
                                                                                     tgcgccaagtgctgcctccgtacgccaagatctccgacgacgcccangaagtnatccaag 249
                                                                                                                                                                                                                    220 tgcggcgcgtgctgccggcgcacgccaagatctcggacgacgccaaggagacgatccagg
 DB 21; Length 622;
14.2%; Score 166.2; DB 21; Length 70.2%; Pred. No. 1e-22; cive 0; Mismatches 101; Indels
                                  Matches 245; Conservative
               Local Similarity
 Query Match
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Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or managany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeodomain/homeodomain zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements

New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide

WPI; 2000-579369/54.

Claim 1; Page 576; 747pp; English.

; 0

Gaps

/ Match 13.1%; Score 154.2; DB 21; Length 470; Local Similarity 71.1%; Pred. No. 1.7e-20; nes 204; Conservative 0; Mismatches 83; Indels 0;

Query Match Best Loca Matches

Sequence 470 BP; 129 A; 114 C; 138 G; 89 T; 0 other;

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Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocic; homeodomain; homeocox; MADS; homeodomain zipper; LIM domain; AP2; ERBBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MXB; ss.
                                                   337 gggagcagcgcaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggct 396
                    310 ccgagcgccgcaagaccgtcacctccgaagacatcgtgtgggccatgagccgcctcggct 369
                                          430 acgggggtgaaaacgcggcggcctgcanggggtngtggtcncgccgcgg 478
                                                                                   457 acgegegegegteggetegteceggggggeegeecategeggegg
                                                                                                                                                                                                                       Pinus radiata transcription factor DNA sequence #503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenk MA, Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                         AAC57057 standard; DNA; 470 BP
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                                                                                                                                                                                                    (first entry)
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18-AUG-1999;
                                                                                                                                                                                                                                                                                                          Pinus radiata.
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agtacatcagettcatcacgggggaggccaacgagcggtgccagcgggagcagcgcaaga 351
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                                                                                                                                                         tecgegageaggaceggetgatgeegategegaacgtgateegeateatgeggegegtge 231
                                              ccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacgtcg
                                                                                                                                                                                                       412 agccgctcggcgcctacctccaccgctaccgcgagttcgagggcgac
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Pinus radiata transcription factor DNA sequence #443.
AAC56997 standard; DNA; 561
         25-JAN-2001 (first entry)
    AAC56997;
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Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocloi; homeodomain; homeoclox; MADS; homeodomain zipper; LIM domain; AP2: EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.

Pinus

WO200053724-A2.

14-SEP-2000

11-MAR-1999;

09-MAR-2000; 2000WO-US06112

99US-0266513, 99US-0149485. 18-AUG-1999;

Glenn M (FLET-) FLETCHER CHALLENGE FORESTS LTD McGrath A, Shenk MA, Wood M,

(GENE-) GENESIS RES & DEV CORP LID

WPI; 2000-579369/54

New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide

## Claim 1; Page 562; 747pp; English.

The present invention relates to movel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2

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EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
            MYB
             and
 22 x 33
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Sequence 561 BP; 145 A; 151 C; 152 G; 113 T; 0 other;

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238 tgcgggagcaggacaggttcctacccatcgccaacattagccgcatcatgaagaaggcgc 297
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                                                                                                                                                                        agtacatcagetteatcaegggggaggecaaegageggtgecagegggageageaga 351
                                                                                                                                                                                                                                 411
                                                                                                                                                                                                                                                          477
                                                          tccgcgagcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgc 231
                                                                                                                                                                                                 358 aatttatcagcttcatcaccagcgaggccagtgacaaatgccagcgagaaaagaggaaga 417
                                Gaps
                                                                                                                                                                                                                           tgccggcgcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgg
                                                                                                                                Score 154.2; DB 21; Length 561;
Pred. No. 1.7e-20;
0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                                                      458
                                                                                                                                                                                                                                                                                                                478 agcccttgaaggtttacttgctcatgtacagagaggcggagggtgac
                                                                                                                                                                                                                                                                                      412 agccgctcggcgcctacctccaccgctaccgcgagttcgagggcgac
13.1%;
71.1%;
                             204; Conservative
              Similarity
  Query Match
Best Local 3
                             Matches
                                                         172
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Search completed: October 25, 2001, 12:29:39 Job time: 3843 sec

Fri Oct 26 14:34:29 2001

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 25, 2001, 09:21:45; Search time 9.89 Seconds (without alignments) 962.894 Million cell updates/sec

US-09-435-054-2
1514
1 MDSSSFLPAAGAENGSAAGG.....ASHTPQGSGGLEHPHPFAYK 278 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

93435 Total number of hits satisfying chosen parameters:

93435 seqs, 34255486 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

			P25209 zea mays (m	5210 petr	-	_		D13434 carcharomic			P25211 venomis lac			P54843 mus musculu	_				2000	-	-			OFOSA GLOSOPHITA	TOURS SAF	D17816 hordows tae			2 11112	 	DE MACO	n c	to mas m		750	
SUMMARIES		ID	CBFA_MAIZE	CBFA_PETMA	CBFA HUMAN	CBFA_MOUSE	CBFA CHICK	HAP3_YEAST	PHP3 SCHPO	HAP3 KLULA	CBFA XENLA	DR1 ARATH	MAF2 RAT	MAF2_MOUSE	HMDF_DROME	TMAF_AVIS4	TBAP HUMAN	FXB2 MOUSE	DRPL HUMAN	BR3A MOUSE	BR3A HIMAN	DRPL RAT	DSX DROME	FXD2 HUMAN	ANX7 XENTA	GRP HORVII	FXGA CHICK	FXC1 MOUSE	ANDR DANTE	ANDR MACEA	ANDR HIMAN	MRG1 MOIISE	FXD1 HIMAN	,	POXM_DROME	
	į	DB	Н	Н		-	П	1	+4	П	Н	Н	Н	щ	7	Н	-	-	щ	~	П	Н	Н	٦	Н	ı <del>, .</del>	Н	-		-	-	-		-	-	
		Length	179	209	207	207	151	144	116	205	122	159	369	. 370	290	369	176	428	1185	421	423	1183	549	497	512	200	440	553	911	895	919	269	465	895	402	
æ	Query	Match	25.8	Н	21.4	21.4	Ξ.	19.5	18.1	17.5	15.4	•	11.8		11.3												8.5									
		Score M	391	<u>ب</u>	'n.	s.	322				232.5	195	79					149	147	139	139	135.5	134	132.5	132.5	129.5	129	129	127.5	124.5	124.5	123.5	123.5	123.5	123	
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P03211 epstein-bar Q61345 mus musculu O97776 eulemur ful O95409 homo sapien P34092 dictyostell O09112 mus musculu Q10571 homo sapien P23118 strongyloce P2582 drosophila P12107 homo sapien Q08473 drosophila Q63410 rattus norv
EBN1_EBV FXD1_MOUSE ANDR_EGULFC 21C2_HUMAN WYSE_DICDI DUSB_MOUSE MN1_HUMAN BIND_STREN FUM_DROME CA1B_HUMAN SQD_DROME OTX1_RAT
ппенененене
641 456 884 833 1111 663 1319 485 1533 1806 345
8.7.7.7.9 7.7.7.8 7.7.7.8
121.5 120 120 119.5 118 117.5 117.5 117.5 117.5 116 116 116 115.5
688888844444 4886788904444

## ALIGNMENTS

CILIGUMENTO	RESULT 1 CBFA_MAIZE LD CBFA_MAIZE STANDARD; PRT; 179 AA. AC P55209:		os dea mays (Maize). OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; OC Magnoliophyta; Liliopsida; Poales: Poaceae: Dack clade: Daniosida;		KN L1 RP SEQUENCE FROM N.A. RX MEDITANE-03105000. D.				<del>!</del> :	COMPONENTS,	CC -1- DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED A CC DOMAIN: THE HIGHLY CONSERVED B DOMAIN TECHNOLOGY TO THE MIGHLY CONSERVED B DOMAIN TECHNOLOGY	-		This SWISS-PROT entry is copyright. It is product between the Swiss Institute of Bioinformation			entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch						The following the following the following of the following	DOMAIN 120 179 CD DNA RIND 36 47 PW	SEQUENCE 179 AA; 18995 MW;	
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209 AA; 22676 MW; E89B0F0289882350 CRC64;

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-I. FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOMIZING AND BINDING TO A CCAAT MOTTE IN PROMOTERS, FOR EXAMPLE IN TYPE I COLLAGEN, ALBUMIN AND BETA-ACTIN GENES.

-I. SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONEWRY, A AND B, THAT ARE BOTH NEEDED FOR DNA BINDING.

-I. SUBCELLULAR LOCATION: UNCLEAR.

-I. DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED A DOMAIN: CAN BE DIVIDED INTO THREE DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GLU-RICH C DOMAIN.

-I. SIMILARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               125 REFEGDARGVGLVPGAAPSRGGD-----HHPHSMSPAAMLKSRGPVS-GAAMLPHHHH 176
                                                                                                                                                                                                                                                                                                                               119 REMEGDSK-----LTAKSSDGSIKKDALGHVGASSSAAEGMGQQGAYNQGMGYMQPQYH 172
                                                                                                                                                                                                                                                                                          65 AKETIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRY 124
                                                                             Gaps
                                                                                                                                             8 PAAGA---ENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDD 64
                                                                                                                                                                                                                   8 PGGGGGSHESGSPRGGGGGG-----SVREQDRFLPIANISRIMKKAIPANGKIAKD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CCAAY-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; DNA binding; Activator; Nuclear protein. DOMAIN 1 53 A DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evolutionary variation of the CCAAT-binding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li X.-Y., Mantovani R., Hooft van Huijsduijnen R., Andre I., Benoist C., Mathis D.;
Query Match 25.8%; Score 391; DB 1; Length 179; Best Local Similarity 44.6%; Pred. No. 3.4e-19; Matches 82; Conservative 31; Mismatches 45; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DOMAIÑ.
B DOMAIN.
C DOMAIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92195809; PubMed=1549471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000947; -.
Pfam; PF00808; CBFD_NFYB_HMF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0615; CCAATSUBUNTA.
PROSITE; PSO0685; CBFA_NFYB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X59712; CAA42232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P19267; 1BFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 HHDM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 NGDI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBFA_PETMA
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DOMAIN
DNA_BIND
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                                        ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Intron-exon organization of the NF-Y genes. Tissue-specific splicing
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NUCLEAR TRANSCRIPTION FACTOR Y SUBUNIT BETA (NF-Y PROTEIN CHAIN B)
BOX DNA BINDING PROTEIN SUBUNIT B).
                                                                                                                                                                                   71 ECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCCIOL STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOGNIZION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOGNIZING AND BINDING TO A CCART MOTIF IN PROMOTERS, FOR EXAMPLE IN TYPE I COLLAGEN, ALBUMIN AND BETA ACTIN GENES.

-: SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONENTS, A AND B, THAT ARE BOTH NEEDED FOR DNA BINDING.

-: OMPRONENTS, A AND B, THAT ARE DOMAINS: THE WEAKLY CONSERVED DOMAIN: THE HIGHLY CONSERVED DOMAIN: THE HIGHLY CONSERVED DOMAIN THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GLU FICH C DOMAIN.
                                        Gaps
                                                                               11 GAENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Evolutionary variation of the CCAAT-binding transcription factor
                                                                                                      12 GDAEGSLASGDHDESCGSK---DPYREQDIYLPIANVARIMKTSIPSSGKIAKDAKECVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                        .,
ښ
21.5%; Score 325.5; DB 1; Length 209; 53.2%; Pred. No. 7e-15; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92195809; PubMed-1549471;
Li X.-Y., Mantovani R., Hooft van Huijsduijnen R., Andre I.,
Benoist C., Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li X.-Y., van Huijsduijnen R., Mantovani R., Benoist C.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Badder Clarke J., Ting J.P.Y.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modifies an activation domain.";
J. Biol. Chem. 267:8984-8990(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92250488; Pubmed=1577736;
                       Local Similarity 53.2%
hes 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                          149 EKGI 152
                                                                                                                                                                                                                                                 131 ARGV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEYB OR HAP3
                                                                                                                                                                                                                                                                                                                                                                                          CBFA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mathis D.;
Query Match
                                                                                                                                                                                                                                                                                                                                                                         CBFA_HUMAN
                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Intron-exon organization of the NF-Y genes. Tissue-specific splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 AIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Co-evolution from yeast to mouse: cDNA cloning of the two NF-Y (CP-1/CBF) subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN B).
                                                                                                                                                                                                                                                                                                             Transcription regulation; DNA-binding; Activator; Nuclear protein.

1 52 A DOMAIN.
DOMAIN. 53 142 B DOMAIN.
DOMAIN. 143 207 C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse), and Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evolutionary variation of the CCAAT-binding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Hooft van Huijsduijnen R., Mantovani R., Benoist C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%; Score 324.5; DB 1; Length 207; 56.6%; Pred. No. 8.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-Mouse;
MEDLINE=92195809; PubMed=1549471;
Li X.-Y., Mantovani R., Hooft van Huijsduijnen R., Andre I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 8.1e-15;
7: Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

1ADFA0E45F3CF972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 20:1087-1091(1992).
                                                     EMBL; X59710; CAA42230.1; ALT_INIT.
PIR; S22817; S22817.
HSSP; P19267; 1BFM.
                                                                                                                               TRANSFA; T00154; --
MIM; 189904; --
InterPro: IPR000947; --
Pfam; PF00808; CBFD_NFYE_HMF; 1.
PRINTS; PR00615; CCAATGUBUNTA.
PROSITE; PS00685; CBFA_NFYB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modifies an activation domain.";
J. Biol. Chem. 267:8984-8990(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91006004; PubMed=1698608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92250488; PubMed=1577736;
                                                                                                                                                                                                                                                                                                                                                                   53 142 B
143 207 C
59 65 BY
207 AA; 22831 MW;
                             EMBL; L06145; AAA59930.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 9:3119-3127(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benoist C., Mathis D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBFA_MOUSE
P22569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mathis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
g
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                                                                                                                                                                      THE HAP3 TEARISTIC CEAST. ASSISTANCE AND ASSISTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 AIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEXISFITGEANERCQREQR 93
                                                                                                    Vuorio T., Maity S.N., de Crombrugghe B.;
"Purification and molecular cloning of the 'A' chain of a rat
hereomeric CCAAT-binding protein. Sequence identity with the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; DNA-binding; Activator; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 21.4%; Score 324.5; DB 1; Length 207; 1 Similarity 56.6%; Pred. No. 8.1e-15; 64; Conservative 17; Mismatches 29; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
; 1ADFB4B04A3CFC22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GBFA_CHICK STANDARD; PRT; 151 AA. P52507; 01-MAY-1992 (Rel. 22, Created) 01-MAY-1992 (Rel. 22, Last sequence update)
                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A DOMAIN.
B DOMAIN.
C DOMAIN.
                                            SPECIES=Rat;
MEDLINE=91093096; PubMed=2266139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:97317; Nfyb.
InterPro; IPR000947; --
Pfam; PF00808; CBFD_NFYB_HMF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X55316; CAA39024.1; --
EMBL; M5645; AAA40887.1; --
EMBL; A20553; CAA01509.1; --
PIR; A21645; S12045.
PIR; A23692; A23692.
PIR; F38245; F38245.
HSSP; P19267; 1BFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00615; CCAATSUBUNTA.
PROSITE; PS00685; CBFA_NFYB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 142 B
143 207 C
59 65 BY
207 AA; 22787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T00613; -. TRANSFAC; T00616; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
SEQUENCE
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Best Local 9
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                              NUCLEIC ACIDS RES. 20:1087-1091(1992).

-I. FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOGNIZING AND BINDING TO A CCAAT MOTIF IN PROMOTERS, FOR EXAMPLE IN TYPE 1 COLLAGEN, ALBUMIN AND BETA-ACTIN GENES.

-I. SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONENTS, A AND B. THAT ARE BOTH NEEDED FOR DNA BINDING.

-I. SUBCELLULAR LOCATION: UNCLEAR.

-I. DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED A DOMAIN; INTERACTION AND DNA BINDING, AND THE GIGHLY CONSERVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GIU-RICH C DOMAIN.

-I. SIMILARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |||| :||||| |||| ||| :|| ||| :|||| :||||| :|||| ||| :||| ||| ||| ||| ||| ||| ||| ||| 49 SFREQDIYLPIANVARIMKNAIPQTGKIAKDAKECVQECVSEFISFITSEASERCHQEKR 108
                                     CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B) (FRAGMENT). Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 AIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00808; CBFD_NFYB_HMF; 1.
PROSITE; PS00685; CBFA_NFYB; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein.
01-NOV-1995 (Rel. 32, Last annotation update)
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN
                                                                                                                                                                                                                                                 'Evolutionary variation of the CCAAT-binding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                           Li X.-Y., Mantovani R., Hooft van Huijsduijnen R., Andre I., Benoist C., Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TRANSCRIPTIONAL ACTIVATOR HAP3 (UAS2 REGULATORY PROTEIN A).
HAP3 OR YBL021C OR YBL0441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.3%; Score 322; DB 1; Length 151; Best Local Similarity 59.8%; Pred. No. 8.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3C2703043DE1A444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 KTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 KTINGEDILFAMSTLGFDSYVEPLKLYLQKFREAMKGEKGIG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DOMAIN.
B DOMAIN.
C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X59713; CAA42233.1; ALT_SEQ.
HSSP; P19267; 1BFM.
                                                                                                                                                                                           MEDLINE=92195809; PubMed=1549471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16733 MW;
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>151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
151 1
151 AA;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P19267,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                          van Dyck L., Pearce D.A., Sherman F., "PIM1 encodes a mitochondrial ATP-dependent protease that is required for mitochondrial function in the yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYCL EMBO J. 12:4647-4655(1993).

-1- FUNCTION: BINDS TO THE UPSTREAM ACTIVATION SITE (UAS) OF THE CYCL GENE AND OTHER GENES INVOLVED IN MITOCHONDRIAL ELECTRON TRANSPORT AND ACTIVARES THEIR ENERRESSION. RECOGNIZES THE SEQUENCE CCAAT.

-1- SUBUNIT: TWO COMPLEXES BIND CCAAT; COMPLEX I, THAT CONSISTS OF HAP2/3/5 AND COMPLEX II, THAT CONSISTS OF HAP2/3/5 AND COMPLEX II, THAT CONSISTS OF HAP2/3/5 AND COMPLEX II, THAT CONSISTS OF HAP2/3/5/4.

-1- SUBCELLULAR LOCATION: NUCLEAR.

-1- DOMAIN: THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INVERACTION AND DNA BINDING, AND THE GLU-RICH C DOMAIN.

-1- SIMILARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goffeau A., Jonniaux J.-L., Purnelle B., Skala J., de Wergifosse
van Dyck L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xing Y., Fikes J.D., Guarente L.; "Mutations in yeast HAP2/HAP3 define a hybrid CCAAT box binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ر.
در
                                                                                           Hahn S., Pinkham J., Wei R., Miller R., Guarente L.; "The HAP3 regulatory locus of Saccharomyces cerevisiae encodes divergent overlapping transcripts."; Mol. Cell. Biol. 8:655-663(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT ASSOCIATION DOMAIN (SAD).
7AB5027BAE420337 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submifted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94038948; PubMed=8223474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 269:238-242(1994).
                                        STRAIN=BWG1-7A;
MEDLINE=88174707; PubMed=2832732;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94103216; PubMed=8276800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pram: Pr00808; CBFD, NFYB_HMF; 1. PRINTS; PR00615; CCAATSUBUNTA. PROSITE; PS00685; CBFA_NFYB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16154 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; T00350;
                                                                                                                                                                                                                                                                                                                       STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DNA_BIND
DOMAIN
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -: SUBCELLULAR LOCATION: NUCLEAR.
-: SUBCELLULAR LOCATION: NUCLEAR.
-: DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED A DOMAIN, THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GLU-RICH C DOMAIN.
-: SIMILARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
8 PAAGAENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKE 67
                    68 TIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYRE 126
                                                                               Brown D., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BELONGS TO A COMPLEX THAT BINDS TO THE SEQUENCE CCAAT
LOCATED UPSTREAM OF GENES INVOLVED IN MITOCHONDRIAL ELECTRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: BELONGS TO AN HETEROTRIMERIC CCAAT-BINDING COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00615; CCAATSUBUNTA,
PROSITE; PS00685; CBFA_NFYB; 1.
DNA-binding; Transcription regulation; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ming Y., Fikes J.D., Guarente L.;
Mutations in yeast HAP2/HAP3 define a hybrid CCAAT box binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DOMAIN.
B DOMAIN.
C DOMAIN.
BX SIMILARITY.
W; 930DFCA773099CB5 CRC64;
                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                      01-00N-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                  116 AA
                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94038948; PubMed=8223474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00808; CBFD_NFYB_HMF; 1.
                                                                                                                                                                                                                                                         TRANSCRIPTIONAL ACTIVATOR PHP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA; 12909 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X75072; CAA52966.1; -. EMBL; Z98559; CAB11161.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 12:4647-4655(1993).
                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
18
                                                                                                                                                                                                                                                                         PHP3 OR SPAC23C11.08.
                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S42744; S42744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P19267; 1BFM.
TRANSFAC; T01263; -
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSPORT
                                                                                                                                                                           PHP3_SCHPO
P36611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain.'
                                                                                                                                                                                                                                                                                                                                                                                                                                        Xing Y
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                                      41 LMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEXISFITGEANERCQREQRKTITAED 100
                                                                                                                                                                                                                                                                                                                                                DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED A DOMAIN, THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBJUNT INTERACTION AND DNA BINDING, AND THE GLU-RICH C DOMAIN. SIMILARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
                    Gaps
                                                       DNA-binding; Transcription regulation; Activator; Nuclear protein.

DOMAIN 21 110 B DOMAIN.
                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Kluyveromyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
IMPORTANT FOR SUBUNIT INTERACTIONS
                 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B33C7B6FBE1D7E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLU-RICH (ACIDIC).
    Pred. No. 8.5e-12;
                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60.5%; Pred. No. o.setive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SER/THR-RICH
                                                                                        101 VLWAMSRLGFDDYVEPLGAYLHRYRE 126
                                                                                                           71 VLLALNTLGFENYAEVLKISLTKYRE 96
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; $1926; $41926.
InterPro; IPR000947; -
Pfam; PF00808; CBFD_NFYB_HMF; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PROSITE; PS00685; CBFA_NFYB; 1.
                                                                                                                                                                                                                                               HAP3 TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                        Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L25779; AAC41662.1; -.
              52; Conservative
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
110
205
33
65
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 AA;
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=28985;
                                                                                                                                                                                 HAP3_KLULA
P40914:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
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                                                                                                                                                                    HAP3_KLULA
              Matches
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Gaps

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25; Indels

17; Mismatches

Conservative

Best Local Similarity Matches 50; Conserv

Matches

18.1%; Score 274; DB 1; Length 116;

Query Match

Query Match

17.5%; Score 265; DB 1; Length 205; 54.3%; Pred. No. 5.7e-11;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 20:1087-1091(1992).

-I. FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOGNIZING AND BINDING TO A CCAAT MOTIF IN PROMOTERS, FOR EXAMPLE IN TYPE I COLLAGEN, ALBUMIN AND BETA-ACTIN GENES.

-I. SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONENTS, A AND B, THAT ARE BOTH NEEDED FOR DNA BINDING.

-I. SUBCELLULAR LOCATION: UNCLEAR.

-I. DOMAIN. THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND BINDING, AND THE GIU-RICH C DOMAIN.

-I. SIBLIARITY: BELONGS TO THE CBF-A SUBUNIT FAMILY.
                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1995 (Rel. 22, Last sequence update)
01-NAY-1995 (Rel. 32, Last annotation update)
01-NAY-1995 (Rel. 32, Last annotation update)
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBE-A) (NF-Y PROTEIN
CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B) (RFAGMENT).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
ZENATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 IQECVSEYISFITGEANERCOREORKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Gaps
               20 LAEQDRWLPINNVARLMKNTLPATTKVSKDAKECMQECVSEFISFVTSEACDRCTSGKRK 79
35 IREQDRIMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00685; CBFA_NFYB; 1. Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                            "Evolutionary variation of the CCAAT-binding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 122;
                                                                                                                                                                                                                                                                                                                                                                             Li X.-Y., Mantovani R., Hooft van Huljsduijnen R., Andre I., Benoist C., Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E76AD9FBC638F53A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 GDARGVGLVPGAAPSRGGD -- HHPH-SMSPAAMLKSRG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 4.4e-09; 14; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 232.5; 50.0%; Pred. No. 4.4
                                                                            95 TITAEDVLWAMSRLGFDDYVEPLGAYLHRYRE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92195809; PubMed-1549471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 AA; 13498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X59709; CAA42229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $22819; $22819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                               CBFA_XENLA
P25211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                 CBFA_XENLA
                                                                                                                                                                              a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuromori T., Yamamoto M.;
"Cloning of cDNAs from Arabidopsis thaliana that encode putative protein phosphatase 2c and a human Dr1-like protein by transformation of a fission yeast mutant.";
Nucleic Acids Res. 22:5296-5301(1994).
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: TO HUMAN PROTEIN DR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 TAEDVLWAMSRLGFDDYVEPL-GAY-LHRYREFEGDARGVGLVPGAAPSRGCDHHPHSMS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 KEDASLPRATWIKIIKEMLPPDVRVARDAQDLLIECCVEFINLVSSESNDVCNKEDKRI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 EQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKTI 96
                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Enkaryota; Viridiplantae; Embryophytta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.9%; Score 195; DB 1; Length 159; 28.0%; Pred. No. 1.5e-06; Live 32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 APEHVLKALQVLGFGEYIEEVYAAYEQHKYETMQDTQRSVKWNPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on; Nuclear protein.
159 AA; 17942 MW; B5BCEC9E9BBF54FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 -AQWTEEEAAAEQQRMF------AEARARMNGGVSVPQPEHP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 PAAMLKSRGPVSGAAMLPHHHHHHDMQMHAAMYGGTAVPPPAGP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF).
                                                                               (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. COLUMBIA;
MEDLINE=95116318; Pubmed=7816619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR000947; ... Pfam; PF00808; CBFD_NFYB_HMF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D38110; BAA07288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                          STANDARD;
                                                                                                                                                                                   PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription;
SEQUENCE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAF2 OR MAF
                                                                                      01-FEB-1996
01-FEB-1996
                                                                                                                                                        01-FEB-1996
                          DR1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAF2 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P54844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
DR1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAF2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                          STRAIN-WISTAR;
MEDLIAE-97190228; PubMed-9038383;
SARAi M., Imaki J., Yoshida K., Ogata A., Matsushima-Hibaya Y.,
Ruboki Y., Nishizawa M., Nishi S.;
"Rat maf related genes: specific expression in chondrocytes, lens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 EDVLWAM-----SRLGF--DDYVEPLGAYLHRYR-EFEGDARGVGLV-----PGAAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 EDYYWMTGYPQQLNPEALGFSPEDAVEALISNSHQLQGGFDGYARGAQQLAAAAGAGAGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SRGGDHHPHSMSPAAMLKSRGPVSGAAM---LPHHHHHDMQMHAAMYGGTAVPPPAGPP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 HHGGFLMPHPQGSSHYLPYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSGSGGGGSA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                             Proto-oncogene, Transcription regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 179; DB 1; Length 369; 30.9%; Pred. No. 3.8e-05;
                                                                                                                          -i- SUBCELLULAR LOCATION: NUCLEAR.
-i- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             288E464708DA6C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                                           POLY-HIS.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
                                                                                                                                                                                                                                                                                                                                              POLY - ALA
                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/C; TISSUE=Cerebellum;
MEDLINE=95097997; PubMed=7799931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                            38457 MW;
                                                                                                                                                                                                                                                                                 EMBL; U56242; AAB50063.1; -.
                                                                                                                Oncogene 14:745-750(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 SHTPQGSGGLEHPH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 GGT-AGAGGALHPH 245
                                                                                                                                                                                                                                                                                                                                                            173
187
194
2220
234
310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                   P05412; 1JUN.
           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                               Nuclear protein.
                                                                                                                                                                                                                                                                                                                                              139
169
180
191
212
225
312
                                                                                                    cord."
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P54843;
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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DOMAIN
                                                                                                  spinal
                                                                                                                                                                                                                                                                                                                                           DOMAIN
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δ
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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                    MAP. Cell. Biol. 15:246-254(1995).

-!- FUNCTION: THE C-MAF INTERACTION SITE WAS MAPPED TO THE SEQUENCE

5'- (GT]G(GC)N(GT)NCTCAGNN-3' IN THE L7 PROMOTER. IT MAY INTERACT
WITH ADDITIONAL BASIC-ZIPPER PROTEINS THAT DETERMINE A SUBTYPE OF

MAF.RESPONSIVE ELEMENT BINDING.

-!- SUBUNIT: HOMO-OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 EDVLWAM-----SRLGF--DDYVEPLGAYLHRYR-EFEGDARGVGLV----PGAAP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 SLGGS--GEEMGPAAAVVSAVIAAAAAQSGAA--PHYHHHHH---HA-----AG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 SRGGDHHPHSMSPA----AMLKSRGPVSGAAMLPHHHHHHDMQMHAAMYGGTAVPPPAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 PPHHGGFLMPHPQGSSHYLPYAYEP-TYGGEHAMAAYYGGAAYAPGNGG---SGDGSGSG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Kurschner C., Morgan J.I.;
"The maf proto-oncogene stimulates transcription from multiple sites
in a promoter that directs Purkinje neuron-specific gene
                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T01432; -.
MGD; MGI:96909; Maf.
Proto-oncogene; Transcription regulation; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 370;
                                                                                                                                           -i - SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEUCINE-ZIPPER.
76A9517EFF9C777C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 176.5; DB 1
33.5%; Pred. No. 5.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HOMEOTIC DEFORMED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-HIS,
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38655 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 GGGGTA----GAGGALHPH 246
                                                                                                                                                                                                                                                                                                          EMBL; S74567; AAB32820.1; -. HSSP; P05412; 1JUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 GGGGSASHTPQGSGGLEHPH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 146
173
187
194
210
220
235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              169
180
191
207
                                               expression."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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   δλ
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EGDARGVGLVPGAAPSRGGDHHPHSMSP 155
                                                                                                                                                                                                                                                                          -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTIFIES ON THE ANTERIOR-POSITENOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Indels 94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulski M., McGinnis N., Chadwick R., McGinnis W.; "Developmental and molecular analysis of Deformed: a homeotic gene controlling Drosophila head development.";
                                                                                                                       Laughon A., Carroll S.B., Storfer F.A., Riley P.D., Scott M.P.; "Common properties of proteins encoded by the Antennapedia complex
                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
"DEFORMED" SUBFAMILY.
                                                                                                                                                                                                                                   "Homeo box genes of the Antennapedia and bithorax complexes of Drosophila.";
Cell 43:71-80(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 171; DB 1; Length 590;
Pred. No. 0.0002;
9; Mismatches 62; Indels
                                                                                                                                                                                               MEDLINE-86079516; PubMed=2416463;
Regulski M., Harding K., Kostriken R., Karch F., Levine M.,
McGinnis W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22407D2562FF24AB CRC64;
                                                                                                                                                            cold Spring Harb. Symp. Quant. Biol. 50:253-262(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTP-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN REF. 3). MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PRO0024; HOMEOBOX.
PRINTS; PRO0025; ANTENNAPEDIA.
PROSITE; PSO0027; HOMEOBOX_1: 1
PROSITE; PSO0032; ANTENNAPEDIA; 1.
PROSITE; PSO071; HOMEOBOX_2: 1.
PROSITE; PSO071; HOMEOBOX_2: 1.
PROSITE; PSO073; HOMEOBOX_2: 1.
PROSITE; PSO073; HOMEOBOX_3: 1.
PROSITE; PSO073; HOMEOBOX_3: 1.
PROSITE; PSO073; HOMEOBOX_3: 1.
PROBING ANTENAPER HEXAPEPTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> I (IN REF. 2).
G -> A (IN REF. 3).
N -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMEOBOX
                                                                                                             MEDLINE=86162966; PubMed=3938363;
                                                                                                                                                  genes of Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63837 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X05136; CAA28782.1; -. EMBL; M13373; AAA28375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%;
30.1%;
                                                                                                 SEQUENCE OF 163-590 FROM N.A.
                                                                                                                                                                                       SEQUENCE OF 366-485 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GFDDYVEPLGAYLHRYREF --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0000439; Dfd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001356; -.
                                                                         EMBO J. 6:767-777(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A24780; A24780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A26638; A26638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02833; 1SAN.
TRANSFAC; T00193; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 71; Conserv
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
456
545
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                              DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM--LPHHHHHHHDMQMHAAMYGGTAVPPPAG 197
                                                                                                                                               ----HHHDMQM----HAAMYGG-----TA 191
                                                  83 ADMVSD-----YMAHHHNPHSHSHSHTHSLPHHHSNSAISGHHQASAGGYSSNYANA 134
                                                                                                              VPP--PAGPPHHGGFLMPHP-QGSSHYLPYAYE------PTYGGEHAMAAYYGGAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90046665; PubMed=2554284; Fujiwara K.T., Kawai S.; Mishizawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai S.; Nishizawa M., Rataoka K., Goto N., Fujiwara K.T., Kawai S.; Proc. Nati. Acad. Oncogene that encodes a 'leucine zipper' motif."; Proc. Nati. Acad. Sci. U.S.A. 86:7711-7715(1989).

-i. FUNCTION: MCHT BE A TRANSCRIPTIONAL TRANS-ACTIVATOR.

-i. SUBCELLULAR LOCATION: NUCLEAR.

-i. DISEASE: INDUCES MOSCULOAPONEUROTIC FIBROSARCOMA IN CHICKENS.
                                                                                                                                                                                                                                                           181 NVPNTSNGGGGGGGGAVLGGGAVGGSANGYYGGYGGYGGYGTANGSVGSTHSQGHSPH 236
                                                                                                                                                                                                                          239 YAP--GNGGSGDGSGS--GGG--GGSAS------HTPQGSGGLEH-----PH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-MAF POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
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F386B220ACE50FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian musculoaponeurotic fibrosarcoma virus AS42.
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01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                369 AA.
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POLY-GLY.
POLY-GLY.
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  156 AAMLKSRGPVSGAAMLPHHH-
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30-MAY-2000 (Rel. 39, Las
TRANSFORMING PROTEIN MAF.
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182
191
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240
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DOMAIN 16
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DNA_BIND
DOMAIN
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MIM; 601482; -.
InterPro; IPR000947; -.
Pfam; PF00808; CBFD_MFYB_HMF; 1.
PFINTS; PR00615; CCATSUBUNTA.
Transcription; Phosphorylation; Nuclear protein.
SIMILAR 100 103 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
nomain 100 103 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
121 168 ALA/GIA-RICH.
121 168 ALA/GIA-RICH.
                                                                                                              -----GGGHPHGAAPGS----APPSSASSSAAGSGGGG 218
139 -AAAAGGSVPAEEMGSAAAVVSAVIAAAAAQGGAPHYHHHHH--------- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inostroza J.A., Mermelstein F.H., Ha I., Lane W.S., Reinberg D.;
"Dri, a TRAP-binding protein-associated phosphoprotein and inhibitor
of class II gene transcription.";
cell 70:477-489(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                           TBAP_HUMAN STANDARD; PRT; 176 AA.

Q01658;
Q01-JUL-1993 (Rel. 26, Created)
Q1-JUL-1993 (Rel. 26, Last sequence update)
Q1-OCT-2000 (Rel. 40, Last annotation update)
TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (DOWN-REGULATOR OF
                                                                 198 PPHHGGFLMPHPQGSSHYLPYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSGSGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PTM: PHOSPHORYLATION REGULATES ITS INTERACTION WITH TBP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-92354065; PubMed=1339312;
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                                                                                                                               180 HPHHGG-----GGG-----
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219 GGG---GGAGGLHHPH 231
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                                                                                                                                                                                                 258 SASHTPQGSGGLEHPH 273
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Best Local Similarity
Matches 35; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC; T00197; -. MIM; 601482; -.
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QY 91 EQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAAPSR 144
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Db 61 SEKKTISPEHVIQALESLGF-----GSYISEVKEVLQECKTVALKRRKASSR 107
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Search completed: October 25, 2001, 09:24:50

Job time: 185 sec

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us-09-435-054-2.p2n.rge

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B0117 : AB025628 Arabidopsis thaliana 826 : A8025628 Arabidopsis thaliana 626 : Ac013482 Genomic sequence for 874 : x13724 Arabidopsis thaliana mRN 197976 : AL161539 Arabidopsis thaliana 141808 : AP003266 Oryza sativa chromo 179686 : AP003246 Oryza sativa chromo 179686 : AP003446 : AP004446 : AP004446 : AP004446 : AP004446 : AP004446 : AP004446 : AP00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A F041204 Xenopus laevis nuclear X59712 P.marinus mRNA for CAAT-M06017 Rat CCAAT binding transc 4 1.06145 Human CCAAT binding transc 4 1.05145 Human CCAAT binding transc 1.05710 H.sapiens mRNA for CAAT-M59710 H.sapiens mRNA for CAAT-M55316 M.musculus mRNA for CAAT-M2053 NF-YB. 6/1994 A 2005317 Homo sapiens, nuclear 11 180005317 Homo sapiens, nuclear 11 180005316 Homo sapiens, nuclear
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47 AF037602 Schistosoma mansoni n
4628 AL132966 Arabidopsis thalian
6514 AC000106 Sequence of BAC F7G
1809 AP003271 Oryza sativa chromc
5 A91200 Sequence 3 from Patent W
25 I 235782 S.cerevisiae Ghromcome
61 M20318 S.cerevisiae HAP3 locus
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8 i AL433029 T7 end of clone BBOAAC

766 i AC0014976 Drosophila melanogas

234 i AE000366 Arabidopsis thaliana

6340 i AE003664 Drosophila melanoga

25 i X75072 S.pombe PHP3 mRNA. 11/71

99 i L25779 Kluyveromyces lactis (H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141808 i AP003266 Oryza sativa chromo
179686 i AP003246 Oryza sativa chromo
870 i X59714 Z.mays mRNA for CAAP-box
832 i Y13723 Arabidopsis thaliana mRN
107377 i AC005309 Arabidopsis thaliana
82403 i AC007063 Arabidopsis thaliana
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AL438685 T3 end of clone XBC0A
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                                                             Date: Oct 25, 2001 2:23 PM
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Database length: -856060004
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Query: US-09-435-054-2
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9b_pl2:ATCHRIV39
9b_pl2:ATCA1
9b_htg24:Ap003266
9b_htg24:Ap003266
9b_pl4:ZMNFYB
9b_pl1:AC005309
9b_pl1:AC005309
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gb_roo:PATCBFAll
gb_pr10:HUMNFYBSU
gb_ro2:RATCBFAll
gb_ro2:RATCBFAll
gb_ro1:HMNFYB
gb_pr4:A20531
gb_pr7:BC005316
gb_ov:GCNFYB
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gb_pl3:F7Gl9
gb_htg24:AP003271
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gb_in2:aE003664
gb_pl4:SPRNAPHP3
gb_pl4:XSKHAP3A
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gb_pl4:SCYBL021C
gb_pl4:YSCHAP
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gb_sts1:CNS077QN
gb_htg4:AC014976
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gb_pl2:AF250338
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9b_pll:AF036684
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3618 : U35341 Emericella nidulans
179682 : ACO84359 Homo sapiens chr
182972 : ACO23550 Homo sapiens chr
4442 : x59709 x.laevis mRNA for CAA
1003 : AL424722 T7 end of clone XA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL Submitted (02-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Instituted, (02-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamuékazusa.or.jp, 7e1:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaosékazusa.or jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi.bin/agd_graph.cgi?c=MuJ7 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein' protein similarity are described as 'unknown protein' The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://comppio.ornl.gov/grail.1.3/), GENSCAN (Chris Burge, MIT, http://ccm.011.3/), GENSCAN (Chris Burge, MIT, http://ccm.011.3/), GENSCAN (Chris Burge, MIT, http://ccm.011.3/), GENSCAN (Chris Burge, MIT, http://ccm.011.20ol.iastate.edu/cgi.bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MQLS and the 3' clone is MGLS and the 3' clone is MGLS and the 3' clone is MGLS and the 5' clone is MGLS and the 3' clone is MGLS 
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (sites)
Kaneko,T., Katoh,T., Asamizu,E., Sato,S., Nakamura,Y., Kotani,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="DNA-binding protein-like"
join(1723. .1976,2116. .2266,2344. .2417,2508. .2667,
                                                                                                                                                                                                                                                                                               AB025628 80117 bp DNA PLN 27-DEC-2000
Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MNJ7
AB025628 BA000015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structural analysis of Arabidopsis thaliana chromosome 5. XI
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/note="CDS is reported in Acc# AB018117
gene_id:MQL5.29"
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gene_id:MQL5.29"
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/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                               AB025628.1 GI:4589434
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                           gb_htg18:AC084359
gb_htg9:AC023550
gb_ov:XLNFYB
                                                                                                                              qb_sts1:CNS071BW
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VERSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
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CDS

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join(24619. 26247,26400. 26723,26819. 26944,27044. 27166,
27252. 27422,27695. 27820,27896. 28030,28231. 28358,
28444. 28552,28759. 29079,29155. 29304,29383. 29669,
                                                                                                                                                                                                                                                                                                                                                                                    join(17364. 19016,19220. 19540,19635. 19760,19841. 19963, 20046. 20282,20360. 20494,20688. 20815,20899. 21007, 21259. 21546,21762. 21914,21995. .22293,22596. .23076) //note="dbj1BAA99625.1 sgene_dd:MNJ7.7 similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFPHSDARELRDDEMRSEVADMPLSETAKECTIVNEPGIPGVKELDWGSFDADLSVND
GRGFGSYSDRFTELDATAGRLQGKADVAVGGGNLVANDTNTSVGFEDHQGQLHHDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEWRSLDSYNOASOTTVTGQAHDQQVONGHARTTTYHNNSQSSVYDVNNKNOTFKADD
PATOCHGENDESYYANNOQAGNTWOQAGNTWOORDSYNOASOTTSTEERGANDYNORTESPATYDSISERGAGNOVNNLYSTE
SPATOCHGENTTGAGSTTPOHNAVASATVONGELSFENDLYNRQQSVDIRAGKSFONNOLF
SPSVGRSSDRRPPHALVSFGFGGKLIVMKDNNGSLQNTSFGSGGTGGSSTTVLNLAEV
STGSARYSSPGEDSLSYFRATCHIQQSLFPOFTVGGNUSGSKELHWATDERLLGESSNNDF
STGKLLIKMLSGLATSCOYVGKLRSPFGSDASOKETDTPEAAVAKTERFAKKGGTONG
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                                                                                                                                                                                                            AGVTLFQSLFLEGIRLTSPAMATAMPNLAPGLIFFIAMIVGLEKMNLKCVYSKLKILG
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SGACVSFNGWAMKRGPVFVSMFSPFATVISVAFAVLTLGESVSLGSVGGWUMFVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGFGSYSDFFTELDATAGNVQGQAEVAVATGGNLVANDTINTSVGLDNSAGFEQHQGQ
VQHDSGSGQYVDNSQSWENLYPGWKYDASTGQWYQVDGQDATVNSQESYINSTGNWES
VAADNSDVAYLKQSTTSAMAGTAESVSTWNQVSQVGNGYPEHMVFDAQYPGWYYDTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFYVDŤVKÔMALRQLÍPGSPLRTLČLLVAGQPAEVCPTGSSSSMLDNWEENLGITTAN
TYTDDDLVIIIHGDSWMKERGEITAHITCYLLADKNEPPPSEGSRLCIVGADHWKPR
TYASPDAIQFTELLYSKKTLGNOXILLPFOPYKIIYAHMLAEVGKLSTAGYVCOAVI
RCLKTSRSSEVEMWKQFASSLEERIRSHQEGGNLAPAKLVGKLLNSLWGMPPAPHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGNPQVNEYQHQQQEAAKLSYSQSANTMSSLMPPASTEPVHEWGGNGRTMAAHSRSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPDFSKTP1QDQTDSSKDKAPDGVTQVKSTRKVPSSRFSRFGIGILKNTVGKVFPSRS
SNEAKLGNENQFYYDDNLKRWVERGVEPPAEEAALPPPPTSVPFRSNSLGHENKSEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMSPSSGSWSSGSPTPSENSPGIPPVSQGSNOFSARGRMGVRARYVDTYNQGSSSMY
QSPPVQSSKPPIPARAKFFVPAAPASFANDQVMESVSAETRQENSGDEAVVGSAGAPG
PSQASFQSPTPSPIAMQRFPSVDNIRRSGSGTSLNGDLPQSVSRRTASWSGSVNSSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MASASQFLLEDQTDEDFFDKLVDDAYSPTEAQASSSVTELKFDD
ESDSDDIRAFSNLSIGKDPLGGGDGTLNEAILGNDVANEGASGSVGEDEPSSIAPEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MASTADFLLDDQTDEDFFDKLVDDSYTPTASSSAKELKFDDGSDSDBARAFANLSVVDDVLGDGDVALNEAGLGNDVANEGTSGSVGKEEPSSSIAPEAVQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNSDANRLRDVDVVRSEVDDMALTETGKESNIVDGSGSPGVKEVDWGSFYADSSVNDG
                                                                                                                                         /translation="MQFFCVNLYRSVLNLLEERMKTEMIEEMVIVGGLVMVQFVYAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains similarity to unknown protein dbj|BAA90625.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSPTSASTFRPSPLNSSSSSLGEELQEVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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3.672
72.105
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US-09-435-054-2 x AB025628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTSEESCSKESCSMMALALASATELLASHCIDMAEQAGÄDHTCVASTVRSSVDIHSP
GDLMTLTAAAAATALRGEAALKVRQPKESRKNATITPCERSFSDSHWPGENCQFRLEEP
NLPLEGELVQCARNGLQRNKRVCVYINKKSQVMIKLKSKHVGGAFSKKIKCVVYGVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNK I A FVDGTLPRPPEFDPSFRVWSRCNSMVKSWI LNSVTKQ I YKSI LRFNDAAEI WK
DLDTRFHITNLPRSYQLTQQIWSLQQGNMSLSDYYTTLKTLMDDLDGASCVNTCRNCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCSATASVNEHSKIVKFLAGLNDFYSTIRSQIIMKKTIPDLABIYNLLDQDHSQRNIV
TNPTNASAFNVSILSNDQIAVNATRSFQPNSKPKVQCSHCGYTGHTADTCYKIHGYPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSDGALDPAGLVAIAIAHAFALFVGVSIAANISGGHLNPAVTLGLAIGGNITLITGF
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AADPKKGSLGTIAPIAIGFIVGANILAAGPFSGGSMNPARSFGPAVVSGDLSQIWIYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLRTVSNAFTTRSHVGSTASSNSWSTIVPALARFGSIGVLRAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELINDGEKPDASPLVHLLRVSGNYGYVSLCRQLHGYVTKHGFVSNTRLSNSLMRFYKT
SDSLEDAHKVFDEMPDPDVISWNSLVSGYVQSGRFQEGICLFLELHRSDVFPNEFSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AALAACARLHLSPLGACIHSKLVKLGLEKGNVVVGNCLIDMYGKCGFMDDAVLVFQHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEKDTVSWNAIVASCSRNGKLELGLWFFHQMPNPDTVTYNELIDAFVKSGDFNNAFQV
LSDMPNPNSSSWNTILTGYVNSEKSGEATEFFTKMHSSGVRFDEYSLSIVLAAVAALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVPWGSLIHACAHKLGLDSRVVVASALIDMYSKCGMLKHAELMFWTMPRKNLIVWNEM
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KCSLESLSLSNRMR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FATRSSVYPFPQFDFADAHYSPYALSNGDNPGTTIVSEVLDGSNFSSWKIAMFVALDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPREPMKFLSRSWSLSASEISKALAQKQRQQRDLFSVSQNSPRGFFQDVAADPLMAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMNSAGTRRSGRLSKWFHIIKQHTNPSTMRIPRKKDKARVQKAHVHSAVSIAALAAGLA
                                                                                                                                                                                  /product-"formyltetrahydrofolate deformylase-like", complement(joln(3514. .3755,3836. .3893,3983. .4032,4110. .4289,4380. .4773,4852. .5148))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFKHKOKVVHHLRSQNRLLLLL"
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                                                                              /codon_start=1
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CDS

	SerSerPheLeuProAlaAlaGlyAlaGluAsnGlySerAlaAlaG  19   ::::::::                   :: :::	
75286		
19 75336	yGlyAlaAsnAsnGlyGlyAlaAlaGlnGlnHisAlaAlaP 33 	
33	roAlaIleArgGluGlnAspArgLeuMetProIleAlaAsnValIleArg 49 ::::::	
50 75424	IleMetArgArgValLeuProAlaHisAlaLySIleSerAspAspAlaLy 66 	
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83 75524		
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116 75624	oLeuGlyalaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgG 133 	
133 75671	yvalGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHis 149      ::  GGGTTAGCTGCAGTGCTGGGTCCGTT75696	
150 75697	LLeulys160	
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173	ishishishishishsasp 179 	
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SOURCE	thale cress. Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophy Magnollophyta; eudicoryledons; core eudicots; Rosidae; eurosids	ta; II;
REFERENCE AUTHORS TITLE	1 (bases 1 to 826) Lotan, T., Ohto, M., Yee, K.M., West, M.A., Lo, R., Kwong, R.W., Yamaqishi, K., Fischer, R.L., Goldberg, R.B. and Harada, J.J. Arabidopsis LEAFY COTYLEDON1 is sufficient to induce embryo	
JOURNAL MEDLINE REFERENCE AUTHORS	<pre>development in vegetative cells Cell 93 (7), 1195-1205 (1998) 98319234 2 (bases 1 to 826) Lotan,T., Ohto,MA., Yee,K.M., West,M.A.L., Lo,R., Kwong,) Fischer,R.L., Goldberg,R.B. and Harada,J.J.</pre>	

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Direct Submission
Submitted (03-DEC-1997) Plant Biology, University of California,
One Shields Ave., Davis, CA 95616, USA
Location/Qualifiers
                                                                                                                                                                                                                                     /product="CCAAT-box binding factor HAP3 homolog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 gGlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 isProHisSerMetSerProAlaAlaMetLeuLysSerArgGlyProVal 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 SerGlyAlaAlaMetLeuProHisHisHisHisHisAspMetGlnMe 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SeralaalaGlyGlyAlaAsnAsnGlyGlyAlaAlaAlaGlnGlnHisAlaAl 32 ::::::|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 rgIleMetArgArgValLeuProAlaHisAlaLysIleSerAspAspAla 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysGluThrIleGlnGluCysValSerGluTyrIleSerPheIleThrGl 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 46.988
                                                                     1. 826
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                                                                                                                                                                                                                                                                                                                                                               224 t
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                                                                                                       /isolate="Ws-0"
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63.052
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Ratio: 3.146
Percent Similarity: 63.052
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US-09-435-054-2 x AF036684
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                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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complement(7212. .7601)
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Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Leaz, C., Li, J., Liu, A., Liu, J., Liu, S., Wukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thale cress. Arabidopsis thaliana Bukaryophyta; Tracheophyta; Spermatophyta; Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Embryophyta; Core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 82875) PROMANTAE E CHARO.O., Johnson-Hopson,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-NOV-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 82875)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, B., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Tarlumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R. Genomic sequence for Arabidopsis thaliana BAC T26F17 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC013482 82875 bp DNA PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC T26F17 from
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                                                                                                           199 roHisHisGlyGlyPheLeuMetProHisProGlnGlySerSerHisTyr 215
                                                                                                                                               469 .........GGGTTT.............CACGGCCCATCTCATGGC 492
                                                                                                                                                                                                                       216 Leu..... ProTyrAlaTyrGluProThrTyrGlyGlyGluHi 228
                                                                                                                                                                                                                                                                                                                                            228 sAlaMetAlaAlaTyrTyrGlyGlyAlaAlaTyrAlaProGlyAsnGlyG 245
182 tHisAlaAlaMetTyrGlyGlyThrAlaValProProProAlaGlyProP 199
                                                                                                                                                                                                                                                                                   493 CTACCTCCTCCGGGTCCTTATGGTTAT........GGTATGTT 527
                                                                                                                                                                                                                                                                                                                                                                                                  528 GGACCAATCCATGGTTATGGGAGGTGGTCGGTACTACCAA...AACGGGT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 lyserGlyAspGlySerGlySerGlyGlyGlyGlyGlyGlySerAlaSer 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome I, complete sequence.
                                                        451 ......TATGGAGGAAATGGTATT.
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Ecker, J.R.
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LOCUS AC013482
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Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(2361. .2747,2834. .4239,4324. .4420))
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                                                                                                                                                                                                                                                                                       Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA on Nov 30, 1999 this sequence version replaced gi:6403470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unknown; similar to ESTs gb/T21171 and
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CDS

CDS

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COMPLEMENT (join (16811. .17014,17112. .17190,17407. .17772,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKASMSQGSALFRIAASVFTEVPNLKMIRDASLGSKNVCFHHAPIFGLVCGLLGMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(13586. 13828,13930. 14008,14146. 14511, 14642. 14984,15072. 15171,15388. 15658,15975. 16084,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAVQVSKKICRVLMIVILFAMMFSAHSNSIDVCVKNCVVNQCMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSPASRKVYNLNDAILRCTIÖVYPRSWTAIYIALDNVGMWNMRSEIWERQYLGQQFYM
RVYTTSTSLRDEYLIPKNALLCGRASSSHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar" to pectinesterase emb|CAB37498.1; similar to ESTs emb|F14)23, gb|T75751, gb|R30156, gb|A1730478.1, gb|A1774044.1, gb|A1726799.1, and gb|A1992516" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Journal of the control of the contro
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                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                            74138 GCCGCCGCTGACAAGAACAATGGTATCGTGCTCCAGCAGCAACCACC 74089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74088 ATGTGGCTCGTGAGCAAGACCAATACATGGCAATCGCAAACGTCATAA 74039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73671 GGACCAATCCATGGTTATGGGAGGTGGTACGAACTACCAA...AACGGGT 73625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73730 ......GGGTTT......GGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 luAspValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 gGlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 isProHisSerMetSerProAlaAlaMetLeuLysSerArgGlyProVal 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 SerGlyAlaAlaMetLeuProHisHisHisHisHisAspMetGlnMe 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 roHisHisGlyGlyPheLeuMetProHisProGlnGlySerSerHisTyr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 tHisAlaAlaMetTyrGlyGlyThrAlaValProProProAlaGlyProP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 Leu.....ProTyrAlaTyrGluProThrTyrGlyGlyGluHi 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 sAlaMetAlaAlaTyrTyrGlyGlyAlaAlaTyrAlaProGlyAsnGlyG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 aProAlaIleArgGluGlnAspArgLeuMetProIleAlaAsnValIleA 49
                                                                                                                                                                                                                                                                                                                                                                 16 SerAlaAlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGlnGlnHisAlaAl 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LysGluThrIleGlnGluCysValSerGluTyrIleSerPhelleThrGl
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                                                                                                                                                                                                                                                                                                                             from: 1 to: 82875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TATGGAGGAATGGTATT.....TATGGAGAATGGTATT
                                                                                                                                                                         Length: 249
Gaps: 9
Percent Identity: 46.988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AC013482
                                                                                                                                                                                                                                                          alignment_block:
US-09-435-054-2 x AC013482/rev
                                                                                                                                                                                             3.146
63.052
                                                                                                                                                                         494.00
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                                                                                                                                                                                             Ratio:
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                                                                                                                                                    alignment_scores:
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FEATURES
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1 (bases 1 to 874)
                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (12-JUN-1997) Edwards D., Plant Sciences, University of
Cambridge, Downing Street, Cambridge CB2 3EA UK
2 (bases 1 to 874)
Edwards, D., Smith, A.G. and Murray, J.A.
Isolation and characterisation of CCAAT box binding proteins from
                                                                                                                                             12-SEP-1997
                                                                                                                                                                Arabidopsis thaliana mRNA for Hap3b transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 ThrileGlnGluCysValSerGluTyrIleSerPheIleThrGlyGluAl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TCCGGTGGAGGGCAAAACGGAACAACCAGAACGGACAGTCCTCCTTGTC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 etargargvalLeuProalaHisAlaLysIleSerAspAspAlaLysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGlnGlnHisAlaAlaProAl 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 alleArgGluGlnAspArgLeuMetProlleAlaAsnVallleArgIleM 51
                                      73624 CGTCGGGTCAAGATGAATCCAGTGTTGGTGGTGGCTCTTCGTCTTCC 73578
245 lyserGlyAspGlySerGlySerGlyGlyGlyGlyGlySerAlaSer 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 38.683
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                                                                                                                                                                                                                            hap3b gene; transcription factor.
thale cress.
Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: ATHAP3B from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="hap3b"
                                                                                                                                               874 bp
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2.957
61.728
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US-09-435-054-2 x ATHAP3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         higher plants
                                                                                   seq_name: gb_pl2:ATHAP3B
                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                                                                            Edwards, D.
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JOURNAL
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                                                                                                                                                                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicaceae; Arabidopsis.

El (bases 1 to 197976)

Direct Submission

NIFECT Submission

NIFECT Submission

NIFECT Submission

Lemckedmips blochem.mpg de mayer@mips.blochem.mpg de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colley Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 annotation of this entry and other sequences of chromosomes 3, this fragment has an overlap with ATCHRIV38 at the 5' end and an overlap with ATCHRIV40 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCHRIV39 197976 bp DNA pLN 16-MAR-2000 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 GGTGGGGTGCAGTATCACCAACATCATCATTTCTTCACCAGCAGAA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 rGlyGlyAlaAlaTyrAlaProGlyAsnGlyGlySerGlyAspGlySerG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GGTGGCG 518
                                    118 GlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgGlyVa 134
                                                                                                                                                                                                                                                                                      364 AGGG.....AGGCCACAGACTGGTGGTGAGGTCGGAGAGC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 isSerMetSerProAlaAlaMetLeuLysSerArgGlyProValSerGly 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 ATCAGAGAGAT.....GCTGTCGGAGATGGCGGTGGGTTCTACGGTGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 isGlyGlyPheLeuMetProHisProGlnGlySerSerHisTyrLeuPro 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 ...... 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 TyralaTyrGluProThrTyrGlyGlyGluHisAlaMetAlaAlaTyrTy 234
                                                                                                                            101 alLeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValGluProLeu 117
                                                                                                                                                                                          264 TGCTCTGGGCTATGACTACTCTAGGTTTTGAGGATTATGTTGAGCCATTG 313
                                                                                                                                                                                                                                                                                                                                                                                 134 lGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHisProH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 AlaAlaMetLeuProHisHisHisHisHisApMetGlnMetHisAl 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 aAlaMetTyrGlyGlyThrAlaValProProProAlaGlyProProHisH 201
aAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAspV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 CCATATGTATGGAGCCACA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 lySerGlyGlyGlyGlyGlySerAlaSer 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 GTAGCGACAGTGGAGGTGGAGCTGCCTCC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL161539.2 GI:7268147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pl2:ATCHRIV39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
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VERSION
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TYTTALLT WEEHRAYVELEY CTGGECDAAVWEHLOGGSRYTK FLELNEGFDOT
RRHILMLKPIPTIKEAFNAYTODERQRNVKPLTRUDSVARONTSMINEDENAYVAAV
TVRROKPLCTHCGKVGHTIOKCYKVHGYPPGMKTGRTGYTK FNPQLHVQPRMPMMP
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ILNNARALLEVGSTRINTHNYSPSTSTRANDAGTHUNGSYFP
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ASRTSLFDGLDGLEEGRLRASSSXAHDERDNDEALENLODRVSFLKRVCFFHLYN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similarity to simlarity to retrovirus-related polyprotein (retrotransposon Tal-3), Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSEKWIRVAVEELQAMELNKTWSVESLPPDKNVYGCKRNFTIKYNPDGTVERYKARLV
AQGFTQQEGIDFLDTFSPVAKLTSAKMMLGLAAITGWTLTQMDVSDAFLHGDLDEEIF
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AEVENLKALLRSEFKIKDLGPARFFLGLLGCKPSSIPMDPTLHLVRDMGTPLPNPTAY
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SSSALPSIIPPSSNTETQDIDSNAVPITRSKRTTRAPSYLSEXHCSLVPSISTLPPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFGCLCFVSTNAHERTKFTPRARACVFLGYPSGYKGYKVLDLESHSVTVSRNVVFKEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similarity to adenylate cyclase (EC 4.6.1.1) II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contains EST gb:AF067468, AI994518.1, T44124"
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/note="LTR retrotransposon"
17575. .22327
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13070. .13365
                                                                                                                                                                        YPELCRMVDLTANNLATHNL"
complement(10443. .11159)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MELASFLGRALFVSVFLLSAWOEFNDFGEDGGRSAKSLKPKFNA
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complement(join(5668. 5772,5865. 5963,6051. 6140,
6238. 6352,7168. 7235))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MCTLEKRODLFLLTLTGDGEHRFHPDTIATILSLLEGAKSGSTR
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                                                                                                                                                                                                                                                                                                                                        /note="strong similarity to Nicotiana tabacum ORF able to induce HR-likelesions, PATX:G1762945 contains EST gb:A1999161.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similarity to carnitine racemase, Escherichia coli
contains EST gb:H36845, A1992737.1, T76583"
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contains EST gb:A1994308.1, AA394352, H36791, AA395864,
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6238. .6352,7168. .7235))
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/note="c:m:
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/gene="AT4g14420"
                                            /variety="Columbia"
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                                                                                                                                                                                                           5668. .7235
/gene="AT4g14420"
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5668. .72
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  source
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AQAYCEINWLQQLLKDLHIPLTCPAKLFCDKKSALHSSLNPVFHERYKHIELOCHTVR
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17575. 19093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48163 GCGGATTCGGACAACGATTCAGGAGGACACAAAGACGGTGGAAATGCT.. 48210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrileThrAlaGluAspValLeuTrpAlaMetSerArgLeuGlyPheAsp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 lyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHisProHis 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SerAspAspAlaLysGluThrIleGlnGluCysValSerGluTyrIleSe 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 nGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuMetProIleA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 laAsnValIleArglleMetArgArgValLeuProAlaHisAlaLysIle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 rPhelleThrGlyGluAlaAsnGluArgCysGlnArgGluGlnArgLysT 95
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                                                                                                                                                                                                                                             19477. .19551
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21549. .22327
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68.889
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US-09-435-054-2 x ATCHRIV39
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I (basea I to 20606)

Bevan, M., Stiekema, W., Murphy, G., Wambutt, R., Pohl, T., Terryn, N., Kreis, M., Kavanagh, T., Entian, K.D., Rieger, M., James, R., Puladdomenech, P., Hatzopoulos, P., Obermaler, B., Duesterhoft, A., Jones, J., Palme, K., Ansorge, W., Delseny, M., Bancroft, I., Unpublished
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EVA Arabidopsis sequencing, project.

EVA AVA TON-1999) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Eval:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATFCA1 206606 bp DNA PLN 29-JUN-1999 Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment
                                                                                                                                                                                      152 SerMetSerProAlaAlaMetLeuLysSerArgGlyProValSerGlyAl 168
                                                                                                                                                                                                                                                                                                                                                                                  48597 TGGCATGGTGACTACGATGGGACATCAATTTTCCCATCAT 48636
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                                                                                                                                                                                                                                                                                                                    168 aAlaMet.....LeuProHisHisHisHisHis 178
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RKQSGYGGQTKPVFHKKAKTTKKIVLRLQCQSCKHFSQRPIKRCKHFBIGGDKKGKGT	Sour Couplement(745828) //www.hor=1	complement(829903) /gene="d13200c"	/ number=2 compler=2 /number=2	//unimical_2 complement(10531232) /gene="d13200c"	/number=3 complement(12331803) /number=3	complement(18041806)	//lumber=4 22292837 /gene="d13205w" /numba=4	//uumber=1 2229734 /	/gene="d1320bw" join(2229. 2837,29143069,31613268,33583468, 35694957,50005212,63406428,64696560.67066749,		/note="similarity to kinesin osm-3, Caenorhabditis ⊝legans	contains EST gb:496806"  /codon_state=1	/protein_id="cAB10212.1"	/db_xref="GI:2244790" /db_xref="SPTREMBL:023291"	/translation="MAPTPSSSRSNQTQYTLIRTPQTKQRLNFHSKTPNPDGSKDPSP PEHPVEVIGRIRDYPDRKEKSPSILOVNTDNOTVRVRADVGYRDFTINGVSFSRORGI.		DOCOVITY OF VITUALISM NEED TO THE STREET OF THE VEHICLE OF THE VEH	NIDQAGQTGFEAKMQTAKINQGNIALKRVVESIANGDSHVPFRDSKLTMLLQDSFEDD KSKILMILCASPDPKEMHKTLCTLEYGAKAKCIVRGSHTPNKDKYGGDESASAVILGS	RIAAMDEFIIKLQSEKKQKEKERNEAQKQLKKKEBEVAALRSLLTQREACATNEEEIK EKVNERTQLLKSELDKKLEECRRMAEEFVEMERRRMEERIVQQQEELEMMRRRLEEIE	VEFRRSNGGSVDETSGFAKRLRSLYSDDDPGMYKSMDLDMGDPEPVKQVWGAVSHQSS NTISSNFTNLLQPKPSENMLTQMYPDRVCLSTVFEEEEVEEEEEKVIVEDKSICLITT	PMPSLNSEGLGRENCFNGADDRESASSRRLRIQNIFTLCGNQRELSQHSGQEEDQANI ASPDKRUNGFSTINKARALAVERKRINISVDQRENGQLDIYKWETAANDRRLIT TIRVTKNATIATIANIKTIFTVICSNOAPPRIKTIKTOTAINOARARATUFU PEROCAAU	AKEKESTVQATSLPLCNGHAYLATLRPGKSSQHKSLQPASPLPLNPIENMEVTPISK	VTPNHQILLKTETERLGEADYINSLSLSHFLILFPRGESHQHRMLSFHSHQTSPSLSS FPLLSRADADEPGLVLDITPLFEVVLEGPTLVLELAVVNDRHIAG"	28382913 /gene="d13205w"	/number=1 29143069	/gene="d13205w" /number=2	30703160 /gene="dl3205w"	//uumber=2 3161. ;328 //ooc=43206:	/ycirc_ discor. /number=3 32693357	/gene="d13205w" /number=3	3583468 /gene="d13205w"	/number=4 34693568 /qene==d13205w"	/number=4 35694957
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Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2001
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Direct Submission
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS
LOCUS
DEFINITION Oryza sativa chromosome 1 clone P0492G09, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0492609
                                                                                                                                                                          102667 GCGGATTCGGACAACGATTCAGGAGGACACAAAGACGGTGGAAATGCT.. 102714
                                                                                                                                                                                                                                                                            102715 ......TCGACACGTGAGCAAGATAGGTTTCTACCGATCG 102748
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                                                                                                                                                                                                                          28 nGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuMetProIleA 45
                                                                                                                           12 AlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGl 28
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                                                                                                                                                                                                                                                                                                                                                                                                                               SerAspAspAlaLysGluThrIleGlnGluCysValSerGluTyrIleSe
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Agrobiological Resources, Rice Genome Research Program; Kannondai 2.1-2, Tsukuba, Ibaraki 305-8602, Japan 12-2, Tsukuba, Ibaraki 305-8602, Japan 12-2, Tsukuba, Ibaraki 305-8602, Japan 12-2, Tsukuba, Ibaraki 307-862, Japan 12-298-38-7441, Fazil-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Location/Qualifiers
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Gaps: 2
Percent Identity: 52.174
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41746 a 30268 c 29643 g 40101 t
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/organism="Oryza sativa"
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                clone P0423A12, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                        1 (sites)
Saski, ... Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0423A12
                                                                                                                                                                                                                                                                Oryza sativa (cultivar:Nipponbare) DNA, clone:P0423A12.
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                                                                                                                            HTG
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
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a 38309 c 38396 g 50748 t
83427 GACCACCCTTCCTCCTCCTCGCCGCCGCC 83459
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
                                                                                                                     AP003246 179686 bp DNA
Oryza sativa chromosome 1 clone
PROGRESS ***, in ordered pieces.
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US-09-435-054-2 x AP003246
                                               seg_name: gb_htg24:AP003246
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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MKKAIPANGKIAKDAKETVQECVSEFISFITSEASDKCQREKRKTINGDDLLWAMATL
GFEDYIEPLKVYLQKYREMEGDSKLTAKSSDGSIKKDALGHVGASSSAAEGMGQOGAY
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Submitted (21-JAN-1992) C. Benoist, L.G.M.E., Dept of Immunology,
Il, Rue Humann, Strassbourg 67000, FRANCE
2 (bases 1 to 0 870)
Li,X.Y., Mantowani,R., Hooft van Huijsduijnen,R., Andre,I.,
Benoist,C. and Mathis,D.
Evolutionary variation of the CCAAT-binding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZMNFYB 870 bp mRNA PLN 09-FEB-1999 Z.mays mRNA for CAAT-box DNA binding protein subunit B (NF-YB).
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/protein_id="CAAA42234.1"
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28085 CGAATCATGAAGCAGATCCTCCCCCCCAACGAGATCTCCCAAGAGGGC 28134
                                                                                                                                                                                                           28335 CCGCCGCCGCCACCTCCCGCTCCGGCGCGCGCCCCCCGCGGGCCCC 28384
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                                                                                                                                                                             82 lyGluAlaAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAla 98
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/db_xref="taxon:4577"
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CAAT-box DNA binding protein.
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alignment\_scores:

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source
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                                                                     AUTHORS
TITLE
    JOURNAL
                                                                                                                                           JOURNAL
                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1373.3.1 GI:2398526
hap3a gene: transcription factor.
haple crees
Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1997
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                                                                                                                                                                                                                                                                                                                                  54 GCGCGCGCGGGGAGCCACGAGAGCGGGAGCCCCAGGGGAGGCGGAGGC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aGluAspValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 CGACGATCTGCTGTGGGCCATGGCCACGCTGGGGTTTGAAGACTACATTG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 luProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAla 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 AACCCCTCAAGGTGTACCTACAGAAGTACAGAGAGATGGAGGGTGATAGC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 ArgGlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAsp.. 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 AAG.....TTAACTGCTAAATCTAGCGATGGCTCGAT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 TAAAAAGGATGCTCTTGGTCATGTGGGAGCAAGTAGCTCAGCTGCAGAAG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 etLeuLysSerArgGlyProValSer...GlyAlaAlaMetLeuProHis 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 GGATGGGCCAACAGGGAGCATACAACCAAGGAATGGGTTATATGCAACCT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                           104 GGTGGCAGCGTCAGGGAGCAGGACAGGTTCCTGCCCATCGCCAACATCAG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 AGCGAAGCGAGTGACAAGTGCCAGAGGGAAAAGCGGAAGACCATCAATGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGluAlaAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAl 98 .::||||||||||::::::::::
                                                                                                                                                                                                                                                                                                                                                                                                   34 .....AlaIleArgGluGlnAspArgLeuMetProIleAlaAsnValIl 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 eArgIleMetArgArgValLeuProAlaHisAlaLysIleSerAspAspA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 laLysGluThrIleGlnGluCysValSerGluTyrIleSerPheIleThr 81
                                                                                                                                                                                                                 6 PheLeuProAlaAlaGlyAlaGluAsnGlySerAlaAlaGly.GlyAlaA 22
                                                                                                                                                                                                                                                            4 TTCCGGATAAGCGCAGGAGGACCTCATGGCGGAAGCTCCGGCGAGCCCTG 53
                                                                                                                                                                                                                                                                                                       snAsnGlyGlyAlaAlaGlnGlnHisAlaAlaPro......33
Length: 191
Gaps: 5
Percent Identity: 42.932
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                                                                                                                                                                 Align seg 1/1 to: ZMNFYB from: 1 to: 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 CAGTACCATAACGGGGATATC 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             832 bp
  392.50
2.784
73.822
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                                                                                                                     US-09-435-054-2 x ZMNFYB
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LOCUS ATHAP3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pl2:ATHAP3A
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       Quality:
                                             Percent Similarity:
                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y13723
                                                                                                alignment_block:
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
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Submitted (12-JUN-1997) Edwards D., Plant Sciences, University of Cambridge, Downing Street, Cambridge CB2 3EA UK
2 (bases 1 to 832)
Edwards, D., Smith, A.G. and Murray, J.A.
Isolation and characterisation of CCAAT box binding proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 AGAAAAGGAAAACTGTGAATGGTGATGTTTGTTGTGGGCCAATGGCAACA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 rArgGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAlaA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 laProSerArgGlyGlyAspHisHisProHisSerMetSerProAlaAla 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 AATGGTAAGATTGGAAAAGATGCTAAGGATACAGTTCAGGAATGCGTCTC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 luGlnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArg 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 LeuGlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTy 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 euMetProlleAlaAsnValIleArgIleMetArgArgValLeuProAla 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 rGluTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 3
Percent Identity: 46.012
                                                                                                                                                                        /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                         /product="Transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                    244 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                        /protein_id="CAA74051.1"
/db_xref="G1:2398527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 832
                                                                                                                                                                                   /db_xref="taxon:3702"
103.528
/gene="hap3a"
/gene="hap3a"
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    204 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: ATHAP3A from: 1
                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                    132 c
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69.939
                                                                                                                                                          1. .832
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US-09-435-054-2 x ATHAP3A
                                                                                               higher plants
Unpublished
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                      252
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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2 (bases 1 to 10737)

2 (bases 1 to 10737)

3 (bases 1 to 10737)

4 (bases 1 to 10737)

5 (bases 1 to 10737)

6 (bases 1 to 10737)

7 (bases 1 to 10737)

8 (bases 1 to 10737)

                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:

LOCUS AC05309 107377 bp DNA PLN 05-APR-2000
DEFINITION Arabidopsis thaliana chromosome II section 254 of 255 of the complete sequence. Sequence from clones T30B22, F17A22, T9J23.

ACCESSION AC005309 AE002093
VERSION AC005309.2 GI:6598453
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158 MetLeuLysSerArgGlyProValSerGlyAlaAlaMet 170
                                                                  478 AATAGAGATGCTGGCGGTGTTTCTGGTGAAAATG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 402 (6763), 761-768 (1999)
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                                                                                                                                                                                                                                                      seq_name: gb_pl1:AC005309
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KEYWORDS
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Submitted (19-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced q1:3738275.
The sequence and annotation of chromosome after removing of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/atc.html).

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orh.lgov/pub/xgrail), Genefinder (Phil Green, University of Mashington), Genscan (Chris Burge, Arthur.epm.orh.lgov/pub/xgrail), searches of the (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes with similarity to cother proteins are named to indicate the level of evidence for their annotation. Genes with similarity are named as 'unknown' proteins. Genes without significant peptide similarity but with EST similarity are named as 'unknown' protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, TRNAscan-SE). Simple repeats were indentified by repeatmasker (Arian Smit, http://ftp.genome.wustl.edu/eddy/RNARpeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael B. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

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join(291. .348,504. .1024,1120. .1549,2112. .2233,2332. .2508)
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GDTLRIRASVATALGAAAAQAKILADQEEREMEQLAATVIEQQLKKLQSKLKFLDDLE
SIMDEEEKVIEGVKETIIQERVSVLQCAFRSGITKRWDHTYVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKKDPLFWNGAILVAPWCKISEKVKPHPIVINLTTRVEBIIPKWKIVPTKDVIDAAFK
DLVKREEVRNNKLIYQDKPRLKTALEMLRTSMNLEDTLHEITWPFFVLHGEADTVTDP
EVSKALYEKASTRDKTLKLYPGMWHALTSGEPDCNVDLVFADIINWLDLRTADPASLT
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/protein_id="AAC63618.2"
/db_xref="GI:6598454"
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TRTPKVYKEYRDFIINKFREDTCRRLTFTSVRKFLVGDVNLLGKVFLELEKWGLINFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLKKNDHLLSVDNAKIEQGTPAGIRVTATPNSLRPITAPPLVEERVETGIKVPPLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSDVFSDLKKPDHVLVCAHCGERCDSPFYQHNKGIVNICEKCFKNGNYGENNTADDFK
LIGNSAAAVWTEEEILLLLESVLKHGDDWELISQSVSTKSRLDCISKLIELPFGEFLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSKPMEEDTNGKTEEEEEVTGPLSVLAMSVKNNTQVLINCRNNR
KLLGRVRAFDRHCNMVLENVREMWTEVPKTGKGKKKALPVNRDRFISKMFLRGDSVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MASLVVEKIYSEVDTCLKLNKLIHVLILECGIRLASAGYAVFGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYEGHGRSMGSRCYIKKFANVVNDCYDYYTSICAQEEYMDKGRFLYGESMGGAVTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4305,4398. .4535,4614. .4712,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTPIRVGNTTSVQRVTTVNGVSNGHRRPKRPFFNLLCGLNRGRLVPRSTV"

join(5465. .5512,5607. .5654,5762. .5786,6120. .6194,

6385. .6489,6572. .6844)

/gene="At2g47640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .4057,4175. .4305,4398. .4535,4614. .4712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5654,5762. .5786,6120. .6194,6385. .6489,
                                                                                                                                                                                                                                         complement(<1. .821)
/note="Sequence from clone T30B22"
join(<291. .348,504. .1024,1120. .1549,2112. .2233,
2332. .>2508)
This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.
                                                                            at@tigr.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Sequence from clone F17A22"
complement(1028. .1102)
/rpt_family="(CAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative phospholipase"
/protein_id="AAC63619.1"
/db_xref="G1:3738277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
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/db_xref="GI:3738278"
                                                                         Address all correspondence to:
                                                                                                                                                                                                       /db_xref="taxon:3702"
                                                                                                   Location/Qualifiers
                                                                                                                                                                          /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /qene="At2q47620"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4788. .>5168)
/gene="At2g47630"
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/gene="At2947640"
                                                                                                                                                                                                                                                                                                                                                                                  <291, ,>2508
/gene="At2g47620"
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/gene="At2g47630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5465. .6844
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                                                                                                                                                                                                                                                                                                                                                        /gene="At2g47620"
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/gene="At2947630"
                                                                                                                                                                                                                               /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="T30B22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="F17A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="F17A22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 822. .107176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(5650.
                                                                                                                      . . 107377
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                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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COMMENT

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VFVLVGIAIATGFTIFSKSSNHQPIPYDVDPLSGYGMRSESSYLPATIHKKPGIEYM
SRIGSAGGKIPLGLKRKVLRVVYGGAGFVGSHLVDRLMARGDNVIVVDNFFTGRKEN
VMHHFNNPNFEMIRHDVVEPILLEVDQIYHLACPASPVHYKFNPVKIIKTNVVGTLNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTSSSSSPITFTLLLLSLLVALNPNPSLASTGSNINTNDIVTO
YSTVYNANAVATVTNPTCVRTLMPFATARNNTSKWARASAVATUTDYRRVLRLLLKTY
ORSAVGESBRIATORNPTSVBLDMLYKSLAVLRTUNADEFGROISDLATWLSAALT
DDDTCLDGFEEFISSRTRTVRMVRRKATKGMRLCSNALALKKLAFDE
                                                                                                                                                                                                                                                                                                                   /translation="MASELTNRRHEIEQPEAESYYPKPIKPWFVAIRPIRYMLREQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(<14085. .14297,14386. .14919,14985. .15179
                                                                                                                                                                                                           /note="The first intron is U12-dependent (AT/AC class)"
comptement(join(6904. .7235,7321. .7413,7965. .8039,
8128. .811,8290. .8369,8740. .8887,8998. .9714))
/gene="At2g47650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTKMKTIEEEEEEERRTSEKGLGREATLIHILPL"
11211. .11254
                                                                                                                                complement(join(7008. 7235,7321. 7413,7965. 80.
8128. 8211,8200. 8369,8740. 8887,8998. 9621))
/gene-"At2947650"
                                                                                                                                                                                                                                              /product."putalive nucleotide-sugar dehydratase"
/protein_id="AAC63621.1"
/db_xref="GI:3738279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="F17A22.5; predicted by genscan"
Join(11209. .11311,11413. .11417)
/gene="At2g47660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8690. .8736
"Ppt_family="(GAA)n"
join(<11209. .11311,11413. .>11417)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 4
Percent Identity: 51.799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative pectinesterase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(<12388. .>13014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<12388. .>13014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(11382. .11410) /rpt_family="POLY_A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(12388. .13014)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(GAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="At2947660"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="At2g47670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At2g47670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="F17A22.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .>11417
                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-435-054-2 x AC005309/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
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                 mRNA
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                                                                                                                                             CDS
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18 AlaGlyGlyAlaAsnAsnGlyGlyAlaAla.GlnGlnHisAlaAlaProA 34

to: 107377

from: 1

to reverse of: AC005309

Align seg 1/1

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Furbidopsis thaliana
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 82403)
Lin,X., Kaul,S., Rounsley,S.D., Benito,M.-I., Town,C.D.,
Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
Fujii,C.Y., Mason,T.W., Retchum,K.A., Lee,J.J., Ronning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4558656.
The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence. Sequence from clones T10F5, F13J11.
AC007063.5 G1:6598657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51436
                                                                                                                                                                                                                                                                                                    51385 CATCCGATAAATGCCACAAGGAGAAGCGAAAGACCGTTAATGGAGACGAT 51336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                         84 laAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 uGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgGlyV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 alGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHisPro 150
                                                                                                                                                                             29
                                                                                                                                                                                                                                                                              84
51576 AGTGGTGGT......GGTGGAGGATCAACAGCAAGAAGGAAGCATGA
                                                                                                                                                                                                      51335 ATCTGTTGGGCTATGCCTAATCTAGGGTTTGATGATTACGCCGCCCAGGT
                                                                            34 laIleArgGluGlnAspArgLeuMetProIleAlaAsnValIleArgIle
                                                                                                                                                                          51 MetArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysGl
                                                                                                                                                                                                                                                                           67 uThrIleGlnGluCysValSerGluTyrIleSerPheIleThrGlyGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValGluProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51285 CAAGAAGTACTTACATCGTTACCGAGTTCTCGAAGGTGAG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 82403)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pl1:AC007063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20083487
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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us-09-435-054-2.p2n.rge

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prediction programs including GRAIL

(ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://archur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://www.cbs.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity, that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were defentified by repeatmasker. Anian Smit. http://ftp.genome.washington.edu/RW,Repeatwasker.html). Genes are numbered from the top to bottom of the chromosome.
were identified by a combination of three methods: Gene
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We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the T1GR Bloinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

CDS

This work was supported by the National Science Foundation. Department of Energy and the US Department of Agriculture.

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Address all correspondence to: at@tigr.org
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                    FEATURES
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CDS

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.28420,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPRVQNLYSVIAALPRSWGLTTHVHGRVLDATYQFLFHTEMDLVSVQRREPWLFNNR
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RHHVPPDSNINPSSGAAITSGVRRVYFWGESFRPCPDGESSRNRNIGESSKRRMLVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RILLREWITSLICSKYTQPASLIVYFETLLSSAATTVDEEKGNPSWQPQADFYYLCILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCPDNDKQVMLLSQVSTYWKNNVQMTAVAIDRAMGYRLVSNQAIVRWYFSPENYDQFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANLPVTFRYEYLMAETLFSQILLLPQPPFKTLYYTLVIMDLCKALPGAFPAVVAGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RALFEKISDLDMESRTRLILMFSHHLSNFQFIWPWEEWAFVLDL,PKWAPKRVFVQEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OREVRLSYWDKIKQSIENATALEELLPPKAGPNFMYSLEEGKEKTEEQQLSAELSRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKQTARDMIVWIEETIYPVHGFEVTLTIVVQTLLDIGSKSFTHLVTVLERYGQVFSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MILLEPFIY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSDNEKAN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46830 CAACAACAACAACAACAACA 46802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6551 ATATAGAGACACCGAAGAGAGAGAAGTTAAC......46521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16472 CAGAATCATCATAATTATCAGTTTCAAGAACAAGAC.....CAAAACAA 46429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16751 GGTAACGGTAAGATCTCAAAAGACGCTAAAGAAACCGTTCAAGAATGTGT 46702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46651 GAGAAAAGAGGAAGACCATCAATGGAGATGATATCATTTGGGCTATCACA 46602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46520 ..AGCCCAAAACAACAACAAGACAAGACAACAACAGCAGATTCAACAA 46473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ArgGly 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 ArgLeuGlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisAr 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 gTyrArgGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 GlyAspHisHisProHisSerMetSerProAlaAlaMetLeuLysSerAr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 rgGluGlnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSer 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 gGlyProValSerGlyAlaAlaMetLeuProHisHisHisHisHisH1sA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 nGlyGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgLeuMetProlleAlaAsnVallleArgIleMetArgArgValLeuPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AlaHisAlaLysIleSerAspAspAlaLysGluThrIleGlnGluCysVa 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 lSerGluTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ProAlaAlaGlyAlaGluAsn...GlySerAlaAlaGlyGlyAlaAsnAs 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 82403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 6
Percent Identity: 37.799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-435-054-2 x AC007063/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   icores:
   Quality: 354.50
   Ratio: 2.686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 laAlaProSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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149 c 188 t 188 t
                                                                                                                                                                                                                                                  AF041204 787 bp mRNA VRT 02-DEC-1998
Xenopus laevis nuclear Y/CCAAT-box binding factor B subunit NF-YB
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="nuclear Y/CCAAT-box binding factor B subunit
NF-YB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tempodinae; Xenopus.

1 (bases 1 to 787)

Li,O., Herrler,M., Landsberger,N., Kaludov,N., Ogryzko,V.V., Nakatani,Y. and Wolffe,A.P. Xenopus NF-Y pre-sets chromatin to potentiate p300 and acetylation-responsive transcription from the Xenopus hsp70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-378-1998) Laboratory of Molecular Embryology, National Institutes of Health/NICHD, Building 18T, Room 106, Bethesda, MD 20892, USA
                                             193 AGTTTCAGAGAGAGATATTTATCTTCCCATCGCTAATGTGGCAAGGAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 AlalleArgGluGlnAspArgLeuMetProIleAlaAsnValIleArgll 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 eMetArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note "similar to CBP-A and yeast HAP-3"
179 spMetGlnMetHisAlaAlaMetTyrGlyGlyThrAlaValProProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 145
Gaps: 3
Percent Identity: 49.655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .787
/organism="xenopus laevis"
/db_xref="taxon:835s"
/cell_type="cocyte"
46. .666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1 to: 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter in vivo
EMBO J. 17 (21), 6300-6315 (1998)
                                                                                                                                     46379 ITCCIACCAGIGGAICAICAACCIIII 46353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 787)
Herrler,M. and Wolffe,A.P.
Direct Submission
                                                                                        196 AlaGlyProProHisHisGlyGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                               AF041204.1 GI:3170224
                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                  mRNA, complete cds. AF041204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.987
78.621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AF041204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 340.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-435-054-2 x AF041204
                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AF041204
                                                                                                                                                                                  seq_name: gb_ov:AF041204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                             DEFINITION
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MEDLINE
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DEFINITION
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TITLE
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MEDLINE
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KEYWORDS
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/protein_id="CAA42232.1"
/db_xref="G1:64218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMNFYB 699 bp mRNA VRT 09-FEB-1999
P.marinus mRNA for CAAT-box DNA binding protein subunit B (NF-YB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erratum:[[published erratum appears in Nucleic Acids Res 1992 Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petromyzon marinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-JAN-1992) C. Benoist, L.G.M.E., Dept of Immunology
11, Rue Humann, Strassbourg 67000, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases I to 699)
Li,X.Y., Mantovani,R., Hooft van Huijsduijnen,R., Andre,I.,
Benoist,C. and Mathis,D.
Evolutionary variation of the CCAAT-binding transcription factor
84 AlaAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAs 100
                                                                                                                                                                                                                                                                                                                                                                                     117 euGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgGly 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 :::111 :::443 TAAAGTTGTATCTTCAGAAATTCAGAGGGCAATGAAAGGGGAAAAAGGC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 ValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAsp.....Hi 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 ATTGGTGGTACAGTTACAACAGGAGATGGTCTGGGCGAAGACCTTGCAGA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 sHisProHis...SerMetSerProAlaAlaMetLeuLysSerArgGlyP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AGAACCTTTCACTAGCCAAATACCAGCAGGTTTAATAACCACAGATGGAC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 20 (5), 1087-1091 (1992)
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/db_xref="taxon:7757"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 roValSerGlyAlaAlaMet.LeuProHisHis 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 AGCAACAGAATGTTATGGTTTATACCACATCAT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAT-box DNA binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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SOURCE
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Vuorio,T., Maity,S.N. and de Crombrugghe,B.

Vuorio,T., Maity,S.N. and de Crombrugghe,B.

Purification and molecular cloning of the A chain of a rat
heteromeric CCAAT-binding protein: Sequence identity with the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukāryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATCHFAll 538 bp mRNA ROD 27-APR-1993
Rat CCAAT binding transcription factor-B subunit (CBF-All) mRNA,
                                                                                                                                                                                                                                                       133 GGTGATGCTGAGGGTAGCCTGGCGAGTGGTGATCACGATGAGAGCTGTGG 182
                                                                                                                                                                                                                                                                                                                                        183 ATCGAAA......GACCCGTATCGCGAGCAGGACATCTACCTGCCGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 ysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeuGlyPhe 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 TAGCTAACGTGGCCCGGATCATGAAGACCTCCATCCCATCCTGGGAAG 273
                                                                                                                                                                                                                                                                                                                                                                                   44 lealaAsnValileArgileMetArgArgValLeuProAlaHisAlaLys 60
                                                                                                                                                                                                                                                                                             27 aGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuMetProI 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IleSerAspAspAlaLysGluThrIleGlnGluCysValSerGluTyrIl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 eSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgGluGlnArgL 94
                                                                                                                                                                                                          11 GlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAlaAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAT binding transcription factor-B subunit.
Rat (Sprague-Dawley) liver, cDNA to mRNA.
                                                              Percent Identity: 53.226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chem. 265, 22480-22486 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="liver"
/tissue_lib="lambda-ZAP"
1. .447
                                                                                                                                                                      to: PMNFYB from: 1 to: 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 AATGAAGGGTGAGAAAGGAATC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete cds.
M60617 J05701
M60617.1 GI:203354
                    325.50
3.356
78.226
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117 euGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgGly 133
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                                                                                         152 g
/gene="CBF-A11"
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ORIGIN
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Run on:

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October 25, 2001, 10:47:45; Search time 1233.41 Seconds (without alignments) 14710.169 Million cell updates/sec
                                                                                                                                  2688314
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	AP003266 Oryza sat	AP003246 Oryza sat	AB025628 Arabidops	AF036684 Arabidops	AC013482 Genomic s	X59714 Z.mays mRNA	Y13724 Arabidopsis	X59712 P.marinus m
ID	AP003266	AP003246	AB025628	AF036684	AC013482	ZMNFYB	ATHAP3B	PMNFYB
DB	83	83	12	12	12	15	13	œ
Query Match Length DB ID	17.0 141808	179686	80117	826	82875	870	874	669
Query	7.0	7.0	6.9	5.3	5.1	3.5	2.1	1.8
Ma	1							
Score	199.8	199.8	198.6	179	177.4	158.2	142.2	138.2
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AL161539 Arabidops 297336 Arabidopsis AC016309 Arabidopsis AC014976 Drosophil AC007063 Arabidopsis MG617 Rat CCAAT D M55045 Rat CCAAT D M55045 Rat CCAAT D X5316 Mmusculus AL0553 NF YE G'19 AL433029 T ord of AC00106 Sequence AP001271 Oryza sat AC037602 Schistoso AF001204 Xenopus 1 AF037602 Schistoso AP1200 Sequence 3 Z35782 S.cerevisia M20318 S.cerevisia	Arabidops tinosynne uman CCAAT .sapiens m Homo sapi Homo sapi Porosophil Drosophil Drosophil Luyveromyc Streptomy reptomyce	21-FEB-2001 COUENCING IN 492G09.  yta; Spermatophyta; cartoideae; Oryzeae; some 1, PAC Institute of rogram; Kannondai dna.affrc.go.jp/, etween the contigs ieces is believed gaps between them submitter. This
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ATCHRIV39  ATFCA1  AC005309  AC014976  AC014976  AC014976  AC007063  ATTCRFA1  RATCRFA1  RATCRFA1  RATCRFA1  RATCRFA1  RATCRFA1  GGNEYB  AF0377QN  F7G19  F7G19  AF037602  AF037602  AF037602  AF037602  AF037602  AF037602  AF037602  AF037602  AF037602  AF041204  AF037602  AF037		pyan clone pleces pponba Embry Feal nd Yam nd Yam nd Yam nd Yam 1-298-160 (5-860 (5-860 (5-860) (5-860
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		2.266 E.S. Satt. 1.100pl 1.100
135.8 122.6 122.6 1122.1 11.122 100.4 100.	0. 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7	APO03266 1418 PROGRESS ***, APO03265 APO03266.1 GI: APO0326.2 PASE CVYZA SATIVA (OIVZA SATIVA
00017884397860178843978601788439786017884397860178843978601788439786000000000000000000000000000000000000		RESULT 1 APO03266 LOCUS DEFINITION ACCESSION VERSION KEYRSION KEYRSION TOTHE JOURNAL AUTHORS TITLE JOURNAL TITLE JOURNAL COMMENT

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oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83290 GGGCCTTCGGCGCCTCGACTTCGACGACCTCGACCCATGCGCAGGTACCTCAACA 83349
                                                                                                                                                                                                                                                                                                                                                                                                                                                             83050 AGGGGGAGGCGCCGGATCAGGCGCGCGGGGAGATCATCAAGGAGCAGGACAGGTTGCTGC 83109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83110 CAATCGCGAACGTGGGGCGAATCATGAAGCAGATCCTCCCCCCCAACGCCAAGATCTCCA 83169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0423A12
clone:P0423A12
closed Only in DataBase (2001) In press
2 (bases 1 to 179686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 egegeggeggegaceaceacegeactecatgtegeeageggegatgeteaagteeegeg
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                                                                                                                                                                                                                                                                                                                                       Length 141808;
available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (cultivar:Nipponbare) DNA, clone:P0423A12.
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                                                                                                                                                                                                                                                                                                                                         DB 83;
                                                                                                                                                                                                                                                                                                                                     17.0%; Score 199.8; DB 83; 65.7%; Pred. No. 3.6e-20; cive 0; Mismatches 152;
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                                                                                                      Location/Qualifiers
1. 141808
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http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is MQL5 and the 3' clone is MGC1.
                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                     ., Katoh, T., Asamizu, E., Sato, S., Nakamura, Y., Kotani, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence-not_experimental
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                                                                                                                                                         Structural analysis of Arabidopsis thaliana chromosome 5. XI
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gene_id:MQL5.29"
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Nakamura, Y.
                 Arabidopsis thaliana
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                                                                                                                                                                                 Unpublished
                                                                                               (sites)
                                                                                                                     Kaneko, T
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                 ORGANISM
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                 Submitted (19-EBB-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affcc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Trel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a variable and the accession number will be preserved.

* NOTE: This is a "Working draft," sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28068 CAATCGCGAACGTGGGGGGAATCATGAAGCAGATCCTCCCCCCAACGCCAAGATCTCCA 28127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28188 AGGCCTCCGACAAGTGCCACAAGGAGAAGCGCAAGACGGTCAACGGCGACGACGACGTCTGCT 28247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18248 GGCCTTCGCCCCTCGCCTTCGACGACTCGACCCCATGCGCAGGTACCTCAACA 28307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28308 AGTACCGCGAGCGCGACCGCGCGCCGCCGCCACCTCCCGCTCCGGCGCG 28367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28368 GGGCGGCGGGGGCCCCGACCACCTTCCTCCTCCGCCGCCGCCGCCGCCGCGCG 28427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 atggcggcgctgctcagcagcatgcggcggcggcgatccgcgagcaggaccggctgatgc 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 egategegaaegtgateegeateatgeggegegtgetgeeggegeaegeeaagatetegg 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 aggccaacgagcggtgccagcgggagcagcgcaagaccatcaccgccgaggacgtgctgt 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 gggccatgagccgcctcggcttcgacgactacgtcgagccgctcggcgcctacctccacc 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 gctaccgcgagttcgagggcgacgcgcgcgcgggctcggcccggggggccgccat 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MNJ7.
AB025628 BA000015
AB025628.1 GI:4589434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 83; Length 179686;
                                                                                                                                                                                                                                                                                     * by the finished sequence as soon as it is available and
* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 199.8; DB 83; .65.7%; Pred. No. 3.2e-20; ative 0; Mismatches 152;
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38309 c 38396 g 50748 t
                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="1
                                                                                                                                                                                                                                                                                                                                                      1. .179686
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  Direct Submission
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20046. 20282, 20360. 20494, 20688. 20815, 20899. 21007,
21259. 21546, 21762. 21914, 21995. 22293, 22596. 23076)
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TLLCVFGALAMSVMHSTSISHKEEDDTPIFVFDRDKVVGCIYLLGAVFVLSTNVVLQA
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VVPWGSLIHACAHKLGLDSRVVVASALIDMYSKCGMLKHAELMFWTMPRKNLIVWNEM
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VGPLVGGALAGLIYGDVFIGSYEAVETREIRV"
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NEYRIKPSVEHCCSLIRAMGQRGEVWQAKQVIQEFGFGYDGVAWRALLGACSARKDLK
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KNKIAFVDGTLPRPPEFDPSFRVWSRCNSWVKSWILNSVTKQIYKSILRFNDAAEIWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLDTRFHITNLPRSYQLTQQIWSLQQGNMSLSDYYTTLKTLWDDLDGASCVNTCRNCK
CCSATASVNEHSKIVKFLAGLNDFYSTIRSQIIMKKTIPDLABIYNLLDQDHSQRNIV
                                IMNSAGTRRSGRLSKWFHHKQHTNPSTMRIPRKKDKARVQKAHVHSAVSIAALAAGLA
SYTSEESCSKESCSMMALALASATELLASHCIDMAEQAGADHTCVASTVRSSVDIHSP
                                                                                                                                    NLPLEGELVQCARNGLQRNKRVCVYINKKSQVMIKLKSKHVGGAFSKKIKCVVYGVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MVSVEKLRRRTRKSSKISAEKTPDRTQSSPIPPVPPISSPIQQN
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TPREPMKFLSRSWSLSASEISKALAQKQRQQRDLFSVSQNSPRGFFQDVAADPLMAEN
                                                                                                    GDLMTLTAAAATALRGEAALKVRQPKESRKNATITPCERSFSDSHWPGENCQFRLEEP
                                                                                                                                                                    EISAWPCRKERENSEEVYFGLKTGQGLLEFKCKSKIQKQRWVAGIQSNLRLVSCLEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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gene\_id:MNJ7.7

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.26944,27044. .27166,
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SPYGRSSDRRPPHALVSFGFGCKLIVWRDNGSLQNYSFGSOGLGGSSTTVLIABY
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SRKLLKMLLSLLRIGOYYGKLRSPFGSDASGKFTTPEANVKLFRAFAKKDGIQNG
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OFYVDTVKQMALRQLIPGSPLRTLCLLVAGOPAEVCPTGSSSSMLDNWEEBULGIITAN
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NEMSPSSGSWSSGSPFPSENSFGIPPVSQGSNOFSARGRMGVRRYVUTYNGGSSSWY
OSPPVQSSKPPIPARAKKFFVRAAPASFANDOVMESVSAERRGVRRYVSTVOTYNGGSSWY
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MSPTSASTFRPSPLNSSSSLGEELQEVEL"
120ft (24619 . 226247, 26400 . 26723, 26819 . 26944, 27044 . 2716
27252 . 27422, 775955 . 27820, 27896 . 28030, 28231 . 28358,
28444 . 28552, 287595 . 29079, 29155 . 29304, 29383 . 29669,
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ASGOYYDNSOSWENLYPGWKYDASTGGWFQVDGHDASMNSQESYENSTSNWENVAANN
SDVAYQRQSTASAVAGTVENVSTWNQVSQVSNGYPEHMVFDSQYPGWYYDTIAQEWRS
LDSYNQAFQTTGQANDQQVQNGNSFTAVDHSRESNVHDVYDKNQILRTQKFDIQSQHG
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QFPHSDARELRDDEMRSEVADMPLSETAKECTIVNEPGIPGVKELDWGSFDADLSVND
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/translation="MASTADFLLDDQTDEDFFDKLVDDSYTPTASSSAKELKFDDGSD
                                                                  VNSDANRLRDVDVVRSEVDDMALTETGKESNIVDGSGSPGVKEVDWGSFYADSSVNDG
                                 SDDAKAFANLSVVDDVLGDGDVALNEAGLGNDVANEGTSGSVGKEEPSSSIAPEAVQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29975. .30431)
/note="contains similarity to unknown protein
dbj|BAA90625.1
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/protein_id="BAB09075.1"
/db_xref="GI:9758777"
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Best Local Similarity 78.79
Matches 237; Conservative
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chromosome I, complete sequence.
                                                                                                                             431 ccaccgctaccgcgagttcgagggcga 457
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                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II;
Brassicales, Brassicaceae, Arabidopsis.
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                                                                                              AF036684 826 bp DNA PLN 02-JUL-1998
Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-DEC-1997) Plant Biology, University of California,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lotan,T., Ohto,M.-A., Yee,K.M., West,M.A.L., Lo,R., Kwong,R.W.,
Fischer,R.L., Goldberg,R.B. and Harada,J.J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 gatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgcacgccaagat 250
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Lotan, T., Ohto, M., Yee, K.M., West, M.A., Lo, R., Kwong, R.W.,

Amangishi, K., Fischer, R.L., Goldberg, R.B. and Harada, J.J.

Arabidopsis LEAFY COTYLEDONI is sufficient to induce embryo

development in vegetative cells
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/db_xref="G1:3282674"
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/chromosome="1"
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Best Local Similarity 66.43
Matches 257; Conservative
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AF036684
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SOURCE
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Direct submissable statement of Biology, University of Pennsylvania, 38th Street and Hamilton Walk; Philadelphia, Pennsylvania 19104-6018, USA 4 (bases 1 to 82075)

Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Klan, C., Altefi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Mukharsky, N., Muyao, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Department of Biology, University of Pennsylvania, 38th and Hamilton walk, Philadelphia, PA 19104-6018, USA

S. (bases 1 to 82075)

S. Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Chio, C., Choi, E., Conn, L., Connay, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J., Edmission Policet, Submission Hopson, C., Choo, C., Li, J., Liu, A., Liu, J., Vu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J., Choi, E., Choi, 
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Bakaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Shinn, P., Brooks, S., Buehler, E., Chao, O., Johnson-Hopson, C.,
Khan, S., Kim, C., Altafi, H., Bei, O., Chin, C., Chin, J., Choi, E.,
Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T.,
Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S.,
Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J.,
Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G.,
Federspiel, N.A., Theologis, A. and Ecker, J. R.
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258 CGGTGAAGCCAACGAGCGTTGCCAACGTGAGCAACGTAAGACCATAACTGCTGAAGATAT 317
                                                                                                                                                                                371 gctgtgggccatgagccgcctcggcttcgacgactacgtcgagccgctcggcgcctacct 430
                                                                                                                                                                                                                                                                            318 CCTTTGGGCTATGAGCAAGCTTGGGTTCGATAACTACGTGGACCCCCTCACCGTGTTCAT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC013482 82875 bp DNA PLN 28-JUN-2000 Genomic sequence for Arabidopsis thaliana BAC T26F17 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Nov 30, 1999 this sequence version replaced 9i:6403470.
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FEATURES

CDS

**trna** 

CDS

us-09-435-054-1.rge

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.24104,24201. .24450,24546. .24753,24936. .25167,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /prodein_id="Apri6543.1"
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MCPIPPEGNNYTYALOVKDQIGSFYXFPSLGFHKAAGGFGGIRISSRALIPVPFPTPAD
DYTLLVGDWYKTYNHKDLKAQLDNGGKLPLPDFGILINGRSSGATLNIEPGKTYRLRISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGLONGLINFRLONHTWILLYEVEGRYTTONLE'SSLDVHYGOSYSVLITADOPAKDYYVV
VSSRFTSKILTTTGVLHYSNSVAPVSGPIPDGPIKLSWSFNQARAIRTNLTASGPRPN
PGGSYRYGVINITRTIRLANNIGHIEGEKQRYANNSASRY PADTPLKLJOYKRIDGVY
PGSIEDOPTNGAIFPTTSWANDADFRFYEVEVIENSEDIVOSWHLDGYSFYVVGMELGK
WSPASRKYYNINDALIECTIOYY PRSWTAITIALDINVGWWNMRSEIWERQYLGGQFYM
RVYTTSTRDEYLIPKNALLGGRASSSHR"
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PLOSSCWHPETCSSIGAYITKVLKLKERPLIVUDEDRRRFIFWSFWFUNIVLONISL
RIPVSFMOTIKSLIPPATTYVLQWILVWRKYEDWRIAMSLYPYUGGILLTSIFELSFNV
FGFCAALFGCLATSTRTILAESLLHGYKFDSINTVYYMAPFATMILGLPAFLLERNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAQOGILINGKFPGPDIAAVTNDNLIINVFNHLDEPFLISWSGIRNWRNSYQDGVYGT
TCPIPPGKNYTYALQVKDQIGSFYYFPSLGFHKAAGGFGAIRISSRPRIPVPFPAPAG
DYTVLIGDWYKTNHKDLRAQLDNGGKLPFPDGILINGRGSGATLNIEPGKTYRLRISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQGTYHYGKIKVTRTIKLASSAGNINGKQRYAVNSASFYPTDTPLKLADYFKIAGVYN
PGSIPDQPTHGAIYPVTSVMQTDYKAFVEIVFENWEDIVOTWHLDGYSFFVVGMELGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSAASRKYWINDAVSRCTVOVYPRSWTAIYVSLDNVGMWNLRSELWERQYLGOOFYM
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18036. 18378,18463. 18562,18737. 19007,19646. 19755,
19855. 19998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAVQVSKKICRVLMIVILFAMMFSAHSNSIDVCVKNCVVNQCMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGLONSLNFRIQNHKMKLVEVEGTHTIQTPFSSLDVHVGQSYSVLITADOPAKDYYIV
VSSRFTSKILLITAGVLHYSNSAGPVSGPIPEAPIQLRWSFDQARAIKTNLAASGPRPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to pectinesterase emb|CAB37498.1; similar to cers emb|E14)23, gb|T75751, gb|R30156, gb|A1730478.1, gb|A1774044.1, gb|A1726799.1, and gb|A1992516" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75559. .25480)
/note="similar to phosphate/phosphoenolpyruvate translocator protein gb|AAD20711; similar to EGTS translocator protein gb|AAD20711; similar to EGTS gb|AAB814011.; gb|AAT28274.1, gb|AA660386, db|IC27462, gb|AT7256635.1, db]|AT001755.1, and gb|A1998102.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental/product="T26F17.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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rSPLLDVVQGCHGYLFSRLFCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:6552730"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                              /codon_start=1
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66.1%;
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25259. .254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 256; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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KVEGTRYCKQGWMYFILTRKKSFKSKS"

Complement(8023. 8304)
                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="marngigssggkkngaggfflatlllwuvsvveiaflkriell
wvicgcefepolmnwvrswisendpfevntsvsllhgittsasvyfillnoclakglde
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lalyrnvtirklillicEhHSiFLHVKLERMAGIRDSNTALVKLEWVLNNTAFVFA
RCIPHILITIKLIKDAHKFGKGVELPLALSGMAGMNILNVGLGLDLFHAFRRERSHRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGLEKRVLELQKEAPAAKSENMMLRREFLTQREDLETVMIERDLSTQAAETASKQHLD
IIKKLAKLEAECRKLRILAKTSSSLSSNQSVDSHSDGGRERVEGSCSDSWASSAFISE
LDQIKNEKGGNRSLQGTTSSTEIDLMDDFLEMERLVALPTETQAKNSKDGYELSLMEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLKDÄYQESRVCFQEVDTKLEKLQAEKDELDSEVICCKEAEKRFSLELEAVVGDKIEM
EDELEKMEAEKAELKISFDVIKDQYQESRVCFQEVEMKLEAMKRELKLANESKTQAES
RVTRMEAEVRKERIVSDGLKEKCETFEEELRREIEEKTMIKREKVEPKIKQEDIATAA
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KHSSSSPIISLPKIFALSSLLSRLDLRHRKFHPSSDLDVSTSQEGTVFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12642. .13364
/note="similar to urease accessory protein UREF sp|Q07402"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEEDERRDIVMSRASSCMQWSQWQLLDSILPTGGFAHSFGLEAA
IQTRLVSSPEDLETHIIHVLDNTASLLLPFVYSALKSPDIETWHKLDGILNATLTNQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKASMSQGSALFRIAASVFTEVPNLKMIRDASLGSKNVCFHHAPIFGLVCGLLGMDS
ETSQRAYLFVTLRDVLSAATRLNIVGPMGASVMQHRIAIVTETVLEKWMNREAGEACQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEKIQAEKDDLEREVKCCREAEKRLSLEIEAVVGDKMELEDMLKRVEAEKAELKTSFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKFADCQKTIASLGKQLQSLATLEEFLIDTASIPGSARSVHNKEALLGKDPHECIKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental complement(join(2361. .2747,2834. .4239,4324. .4420)) /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="unknown; similar to ESTs gb|T21171 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unknown; similar to EST gb|AA586241"
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/note="unknown; similar to EST gb|H74506"
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="codon recognized: CAA"
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Location/Qualifiers
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                                                                                                                                                                       /clone="T26F17"
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CDS

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WKALPANGKTAKDAKETVQECVSEFISFITGEASDKCQREKRKTINDDLLAMATL
GFEDVIEPLKVYLQKYREMEGDSKLTAKSSDGSIKKDALGHVGASSSAAEGMGQQGAY
NQCMGYMQPQYHNGDISN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryóta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 870)
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11,20(7):1841]]
                                   74181 GCACAGCAACAACCCCAACCCCAATGACCAGCTCAGTCGTAGTAGCCGGCGCCGGTGACAA 74122
                                                                                                 74061 CATGCCAATCGCAAACGTCATAAGAATCATGCGTAAAAACCTTACCGTCTCACGCCAAAAT 74002
                                                                                                                                                                                                                                                Direct Submission
Submitted (21-JAN-1992) C. Benoist, L.G.M.E., Dept of Immunology,
11, Rue Humann, Strassbourg 67000, FRANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z.mays mRNA for CAAT-box DNA binding protein subunit B (NF-YB). X59714
131 caacaatggcggcgctgctcagcatgcggcggcggcgatccgggagcaggaccggct 190
                                                                                                                                                                                                                              ctcggacgacgacgaggagacgatccaggagtgcgtgtcggagtacatcagcttcatcac 310
                                                                                                                                                                                                                                                                                                    311 99999aggccaacgagcggtgccagcgggagcagcgcaagaccatcaccgccgaggacgt 370
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                                                                                                                                                      gatgccgatcgcgaacgtgatccgcatcatgcggcgcgcgtgccggcgacgccaagat
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/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 ccaccgctaccgcgagttcgagggcga 457
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CAAT-box DNA binding protein.
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-JUN-1997) Edwards D., Plant Sciences, University of Cambridge, Downing Street, Cambridge CB2 3EA UK 2 (bases 1 to 874) Edwards, D., Smith, A.G. and Murray, J.A. Isolation and characterisation of CCAAT box binding proteins from
                                                                        115 cggcggcgggcggccaacaatggcgcgctgctcagcagcatgcggcggcggcgatcc 174
                                                                                                            58 CGCCGCCGCGCCCACCACGAGCCCCCAGGCCAGGCGGAGGCGGTGCCAGCG-TCA 116
                                                                                                                                                   175 gegaggaggaceggetgatgeegategegaaegtgateegeateatgeggegegegtgetge 234
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                                             Gaps
                                                                                                                                                                                                                                                                                                      295 acatcagcttcatcacgggggaggccaacgagcggtgccagcgggagcagcgcaagacca
                                                                                                                                                                                                                                                 237 TCATCTCCTTCATCACTAGCGAAGCGAGGTGACAAGTGCCAGAGGGGAAAGACCGAAGACCA
                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana mRNA for Hap3b transcription factor 13724
     Length 870;
                                       0; Mismatches 108; Indels
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   Score 158.2; DB 15;
Pred. No. 2.7e-13;
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/db_xref="taxon:3702"
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/protein_id="CAA74052.1"
/db_xref="GI:2398529"
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   13.5%;
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                                   Matches 234; Conservative
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SERGHQEKRKTINGEDILFAMSTLGPDSYVEPLKQYLQKYRESHKGEKGINATVYTTT
DAIPBELTEESFSGFPINGTORQQIPGVQPIQFT"
179 c 205 g 129 t
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                                                                                         129 CCGCCAACGCCAAGATCTCTAAAGATGCCAAAGAGACGATGCAGGAGTGTGTCTCCGAGT 188
                                                                                                                                                                                                                              295 acatcagcttcatcacgggggaggccaacgagcggtgccagcgggggggcagcgagagcca 354
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                                                                                                                                                                                                                                                                                                                                                        249 TCAACGGAGACGATTTGCTCTGGGCTATGACTACTCTAGGTTTTGAGGATTATGTTGAGC 308
                                                                                                                                                  235 cggcgcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgtcggagt 294
                       Gaps
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Benoist,C. and Mathis,D.
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Pred. No. 4.6e-11;
0; Mismatches 98; Indels
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1 (bases 1 to 699)
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/db_xref="taxon:7757"
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/db_xref="GI:64218"
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    67.28;
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                          Matches 201; Conservative
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/translation="MELASFLGRALEVSVFLLSAWOEFNDFGEDGGRSAKSLKPKFNA FVHWTTHTAGQLPPVDMKILVAAALALGGLLFVFGSSLGAYLLLLLHQAVATPIL YDFYNYDVDRKEFGQLFSFTGSLALGGLLFFIGMKNSRKHGRQLRKKAFKAFRAN" complement(join5668. 5772,5865. 5963,6051. 6140,6238. 6352,7168. 7235))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

EU (bases 1 to 197976)

EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="strong similarity to Nicotiana tabacum ORF able to induce HR-likelesions, PATX:G1762945. contains EST gb:A199161.1" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemic. Am Kinoferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Biochemic. Am Kinoferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemckedmips. blochem.mpg.de,mayerdmips. biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
this fragment has an overlap with ArCHRIV40 at the 3' end and an
overlap with ArCHRIV40 at the 3' end.
                                                                                                                                                                  229 tgctgccggcgcacgccaagatctcggacgacgacgacgaggagacgatccaggagtgcgtgt 288
                                                                                                               254 CCATCCCATCCTCTGGGAAGATTGCAAAGGACGCCAAGGAGTGTGTGCGAGGAGTGCGTGA 313
                                                                                                                                                                                                                                                                                        agaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacg 408
                                                                                                                                                                                                                                                                                                                                              374 AGACGATCAATGGGGAGGACATCCTCTCGCCATGTCCACCCTTGGCTTCGACAGCTACG 433
194 CGTATCGCGAGCAGGACATCTACCTGCCGATAGCTAACGTGGCCCGGATCATGAAGACCT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCHRIV39 197976 bp DNA PLN 16-MAR-2000
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39.
AL161539
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/variety="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 TCGAGCCGCTCAAGCAGTATCTTCAAAAGTACCGTGAGT 472
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Arabidopsis thaliana
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complement(5773. .5864)

intron

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21549. :22327)
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QPRMGFPAQPTNSMQKANVYAQVYAETGAYPSEGYSQAPMMRYGSYPMPHTHGGN
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VHITQKLILHNVLHVPDFKFNLMSVSSLVKTISCSAHFYVDCCLIQELSQGLMIGRGR
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ILNVARALLEGSNIPMQYWSDCVTTAYFLINRLPSPLLNNKSPYELILNKQPDYSLLK
NFGCLCFVSTNAHERTKFTPRARACYFLGYPRGYPGYKGYKVLLDESHSVYVSRNVYREH
VFPRETSELLNKANDMFDNSILD-LPAPLHFVETMPLIDEDSILPTTOSRTANHASS
SSSALPSIIPPSSNTETQDIDSNAVPITRSKRTTRAPSYLSEYHCSLVPSISTLDPTD
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HNNLASNPFDLVHLDIWGPFSIESIEGFRYFLTVVDDCTRTTWYMLRNKKDVSSVFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSIPIHPLPEIFTASSPKKTTPYPISTVVSYDKYTPLCQSYIFAYNTETEPKTFSQAM
KSEKWIRVAVEELQAMELNKTWSVESLPPDKNVYGCKWVFTIKYNPDGTVERYKARLV
AQGFTQQEGIDFLDTFSPVAKLTSAKMMLGLAAITGWTLTQMDVSDAFLHGDLDEEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKLIGRLLYLTITRPDITYAVHQLSQFISAPSDIHLQAAHKVLRYIKANPGQGLMYSA
DYEICLNGFSDADWAACKDTRRSISGFCIYLGTSLISWKSKKQAVASRSSTESEYRSM
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DOTKAOULKALHVPTENQHADILTKALHPGPFHHLLRQMSLSSLFLPNKPVRS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to simlarity to retrovirus-related polyprotein (retrotransposon Tal-3), Arabidopsis thaliana /codon_start=1
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NGHAAASGLMFALSHDYVFMRKDRGVLYMSEVDIGLPVPDYFSALVVAKVGSGIARRE
LLLSGKKLKGEERAVALGIVDSAAHDSAEGVVEATVSLGESLAAKKWNGEVYATIRKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSILITTANGKFFSNGFDLAWAQTAGSKTGAANRLHQMVESFKPVVAALLLÜLPMPTIA
ALNGHAAAAGLILALSHDYVFMRKDRGVLYMSEVDIGLSMPDYFSALVRAKIGTSAAR
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SLYPELGGLIGLETRVFATPKL"
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/gene="AT4g14440"
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/gene="Ar4g14440"
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complement(f)
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/note="ciminates/"
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/number="
             complement(5865. .5963)
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                                                                                      complement(5964. .6050)
                                                                                                                                     complement(6051, .6140)
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                                                                                                                                                                                                                   complement(6141. .6237)
                                                                                                                                                                                                                                                                                                                                           complement(6353. .7167)
                                                                                                                                                                                                                                                                                                                                                                                       complement(7168. .7235)
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/gene="AT4914430"
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/gene="AT4g14430"
complement(8407. .
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                                                                                                                     /number=2
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complement(join(685.7.744,829. .903,1053. .1232,1804. .1806))
                                                                               complement(join(685. .744,829. .903,1053. .1232,1804. .1806))
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TSTBAGKTSKEIVKVEKRRIVKSTLCNBRSSRSTACIIILDVPTVGGRLMLVDMAGSE
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NIDGAGGTGFEAKMTTAKINGSTAKRVESIANDSHVPFRDSKLTMLLDSFEDD
KSKILMILCASPDPKEMHKTLCTLEYGAKAKCIVRGSHTPNKDKYGGDESASAVILGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MVNIPKTKNTYCKNKECKKHTLHKVTQYKKGKDSLAAQGKRRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="maptpsssrsnotqytlirtpotrorlnfhsktpnpdgskdpsp
pehpvevigrirdypdrkekspsilovntdnotvrvradvgyrdftldgvsfsegegl
EEFYKKFIEERIKGVKVGNKCTIMMYGPTGAGKSHTWFGCGKEPGIVYRSLRDILGDS
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KRKESTVQATSLPLCNGHATLATLRFEKSSQNKKSLQPASPDFNPIENMMEVTPISK
VTPHHQILLKTETBELGEADVINSLSLSHFILLFPRGESHQHRMLSFHSHQTSPSLSS
FPLLSRADADEPGLVLDITPLFEVVLEGPTLVLELAVVNDRHTAG"
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ASPDKKDNQFFSITNKAEALAVEEAKENNISVDQRENGQLDIYVKWETAADNPRKLIT
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3569. .4957,5000. .5212,6340. .6428,6469. .6560,6706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similarity to kinesin osm-3, Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"kinesin like protein"
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                                                                                                                                                                                .744)
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                                                                                                                                                                                complement(685.
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                                                                                                         /gene="d13200c"
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1 (bass 1 to 206606)
Bevan, M., Stiekema, W., Murphy, G., Wambutt, R., Pohl, T., Terryn, N., Kreis, M., Kavanagh, T., Entian, K.D., Rieger, M., James, R., Buidomenech, P., Hatzopoulos, P., Obermaier, B., Duesterhoft, A., Jones, J., Palme, K., Ansorge, W., Delseny, M., Bancroft, I., Mewes, H.W., Schueller, C. and Chalwatzis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (25-JUN-1999) MIPS, at the Max-Planck-Institut fuer
Blochemie Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
schuelle@mips.blochem.mgo.de,mayer@mips.blochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATFCA1 206606 bp DNA PLN 29-JUN-1999
Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment
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                                                                                                                                                                                                                                48162 GGCGGATTCGGACAACGATTCAGGAGGACACAAAGGACGGTGGAAATGCTTCGACACGTGA 48221
                                                                                                                                                                                                                                                                                                                    48402 CGGTGACGATCTTTGGGCGATGACTACGCTAGGGTTTGAGGACTACGTGGAGCCTCT 48461
                                                                                                                                                                                                                                                                                                                                                                                    239 gcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgtcggagtacat 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418
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                                                                                                                                                                              119 ggcgggcggccaacaatggcggcgctgctcagcagcatgcggcggcggcggcgatccgcga 178
                                                                                                                                                                                                                                                                                  Gaps
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                                                                            Length 197976;
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                                                                       Score 135.8; DB 13; Length
Pred. No. 2.6e-11;
0; Mismatches 127; Indels
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1. .26121
/number=4
21549. .22327
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ilarity 62.5%;
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AUTHORS
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JOURNAL
                             exon
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KEYWORDS
SOURCE
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids.II;
Brassicales; Brassicaceae; Arabidopsis.

I (bass 1 to 10737).

RS Lin.X., Kaul.S., Rounsley, S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
Feldilyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,
Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Nietman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 102786 GAACGCAAAAATCTCTAAGGATGCTAAAGAAACGGTTCAAGAGTGTGTATCGGAATTCAT 102845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 102666 GGCGGATTCGGACAACGATTCAGGAGGACACAAAAGACGGTGGAAATGCTTCGACACGTGA 102725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 102846 AAGTTTCATCACCGGTGAGGCTTCTGACAAGTGTCAGAGAGAAGAAGAAGAAAATCAA 102905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102726 GCAAGATAGGTTTCTACCGATCGCTAACGTTAGCAGGATCATGAAGAAAGCACTTCCTGC 102785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggc 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 egecgaggaegtgetgtggggeeatgageegeeteggettegaegaetaegtegageeget 418
                                                                                                                                                                                                                                                                                                                                                                                                                                 119 ggcgggcggcgacaacaatggcggcgctgctcagcagcatgcggcgccggcgatccgcga 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana chromosome II section 254 of 255 of the complete sequence. Sequence from clones T30B22, F17A22, T9J23. AC005309 AE002093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cagetteateacgggggaggecaacgageggtgecagegggageageagaceateae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgtcggagtacat
                                                                                                                                                                                                                                                                                                                                              Length 206606;
                                                                                                                                                                                                                                                                                                                                         11.6%; Score 135.8; DB 13; Length ilarity 62.5%; Pred. No. 2.5e-11; Conservative 0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 102966 CAAGGTTTATCTGCAAAGTATAGGGAGGTGGAAGGAGA 103004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402 (6763), 761-768 (1999)
                                                                                                                                                                                                                                                                                                   complement(7289. .7352)
                                                                                                                                                                                                                                                        complement (7025.
                                                                                                                                               complement (6773.
                                                                                                                                                                                       complement(6888.
                                                                                6750. .7315
/gene="d13210c"
                 6706. .6749
/gene="dl3210c"
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/number=8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(6533. 6772,6888. 7024,7289. 7352,
7451. 7524,7658. 7784,7870. 7954,8046. 8109,8216. 8277,
8489. 8559,8688. 8783,8860. 9008,9099. 9168,9435. 9475,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDRNQRMDHVIGGKFKLGRKLGSGSFGELYLGINIOTGEEVAVK
LEPVKTRHPQLQYESKIYMFLQGGTGVPHLKWFGVEGEYSCMVIDLLGPSLEDLFNYC
KRIFSLKSVLMLADQLICRVEYMHSRGFLHRDIKPDNFLMGLGRRANQVYIIDYGLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WQGLKAGTKKQKYDKISEKKMLTSVETLCKSYPSEFTSYFHYCRSLRFEDKPDYSYLR
RLFRDLFIREGYQLDYVFDWTISKYPQIGSSSRPRPTPRPALDPPGPPAERAEKPTVG
QDLRGRFTGAIEAFTRRNVSSQGALGDRSRHRSSDDIPSSAKEVHESRNGSTSKRGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(6533. .6772,6888. .7024,7289. .7352,7451. .7524,7658. .7784,7870. .7954,8046. .8109,8216.8489. .8559,8688. .8783,8860. .9008,9099. .9168,9435.
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/db_xref="G1:2244791"
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/gene="d13210c"
6533. .qrf
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/gene="dl3205w"
/number=8
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3358. .3468
/gene="dl3205w"
                                                                                                                                                                                                                                                                                                                                                                                                    3569. .4957
/gene="d13205w"
/number=5
/958. .4999
/gene="d13205w"
/number=5
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5213. .6339
/gene="d13205w"
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6429. .6468
/gene="d13205w"
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/gene="dl3210c"
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/qene="dl3210c"
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/gene="dl3205w"
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/gene="dl3205w"
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/gene="dl3205w"
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/gene="dl3205w"
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                 2914. .3069
/gene="dl3205w"
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/gene="d13205w"
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6340. .642
                                                            'number=2
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/product="putative nucleotide-sugar dehydratase"
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join(11209. .11311,11413. .11417)
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/gene="At2g47660"
/note="Sequence from clone F17A22" complement(1028. .1102)
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/note="molecular marker 90J19T7"
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/gene="At2947650"
                                                            /rpt_family="(CAAAA)n"
1216. .1715
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/rpt_family="(GAA)n"
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/gene="At2g47640"
/note="F17A22.3"
                                                                                                                                                /gene="At2g47620"
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/gene="At2g47630"
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/gene="At2g47630"
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                                                                                                                                                                                                                                join(<3826.
4788. .>516
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                                                                                                                                                                                                                                                                                                                                                                        Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.cnn.jgov/pub/xgrail), Genefinder (Phil Green, University of Mashington), Geneson (Chris Burge, http://arthur.epm.cnn.jgov/pub/xgrail), and NetplantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without significant peptide or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscar-ESE (Sean Eddy, Christopherical) and the production or the contraction of their length are predicted by tRNAscar-ESE (Sean Eddy, Christopherical) and the contraction of the contraction or the contraction of the contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(291. .348,504. .1024,1120. .1549,2112. .2233,2332. .2508)
/gene="At2g47620"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jining Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEATDPSAEIELYTIPAQSSWFLWDDIHEIERREFAEFFTESSI
TYFRYVKRYKBYILINKFREDTGRRLFFTSVPRFLYGDVLLQKVFLEEKWGLINFS
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YSDVFSDLKKPDHVLVCAHGGERCDSPFYQHNKGIVNICEKCFKNGNYGENNTADDFR
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SIMDEEEKVIEGVKETIIQERVSVLQCAFRSGITKRWDHTYVK"
822. .107176
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/protein_id="AAC63618.2"
/db_xref="GI:6598454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIGNSAAAVWTEETILLLLESVLKHGDDWELISQSVSTKSRLDCISKLIELPFGEFLM
GSASGRLNPSILTEDENTEQVQTDGQEHEETETREEKEDRVNEDEPPAKRKRVALISE
                                                                Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:3738275. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker: (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<1. .821)
/note="Sequence from clone T30B22"
join(<291. .348,504. .1024,1120. .1549,2112. .2233,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Columbia"
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                                        Direct Submission
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                                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKKDPLFWNGAILVAPMCKISEKVKPHPIVINLLTRVEEIIPKWKIVPTKDVIDAAFK
DLVKREEVRNNKLIYQDKPRLKTALEMLRTSMNLEDTIHEITMPFFVLHGEADTVTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVSKALYEKASTRDKTLKLYPCMWHALTSGEPDCNVDLVFADIINWLDLRTADPASLT
VYPIRYGNYTSVQRVTTVNGYSNGHRRPKRPFFNLLCGLNRGRLVPRSTV"
join(5465. . 5512, 5607. . 5654, 5762. . 5786, 6120. . 6194,
6385. . 6489, 6572. . 6844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"putative small nuclear ribonucleoprotein D2"
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/translation-"WSFPMEBDTNGKTEEEEFNTGPLSVLMMSVKNNTQVLINCRNNR
KLLGRVRAFDRHCNMVLENVREMWTEVPKTGKGKKKALPVNRDRFISKMFLRGDSVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MASELTNRRHEIEQPEAESYYPKPIKPWFVAIRPIRYMLREQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFVLVGIAIATLGFTIFSKSSNHQPIPYDVDPLSGYGMRSESSYLPATIHKKPSIEYM
SRIGSAGGKIPLGLKRKVLRVVVTGGAGFVGSHLVDRLMARGDNVIVVDNFFTGRKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGLAKRVGARFLLTSTSEVYGDPLQHPQVETYWGNVNPIGVRSCYDEGKRTAETLTMD
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SDLVEGLMRLMEGEHVGPFNLGNPGEFTMLELAKVVQETIDPNAKIEFRPNTEDDPHK
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/note="molecular marker mi79a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,v.u(2650. .5654,5762. .5786,6120. .6194,6385. .6489,
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                                                                                                                                                                                                                                                                              .4057,4175. .4305,4398. .4535,4614. .4712,
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8128. 8211,8290. 8369,8740. 8887,8998. 9714))
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QRSAVGESERIALSDCRELFVDSLDNLYKSLAVLRTLNADEFQRQISDLATWLSAALT
DDDTCLDGFEETSSRTRTVRMYRRKATKCMRLCSNALALLKKLAFDGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51347 AATGGAGACGATATCTGTTGGGCTATGGCTAATCTAGGGTTTGATGATTACGCCGCCCAG 51288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 gcgcacgccaagatctcggacgacgacgaggagacgatccaggagtgcgtgtcggagtac 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 gagcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccg 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 atcagetteateaeggggggaggecaaegageggtgeeagegggageagegaeete 356
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This sequence was identified as CDM:10213743 by the submitter.
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                                                                     /db_xref="G1:3738280"
/trab.aralation="MTKMKTIEEEEEEEERTSEKGLGREATLIHILPL"
11211. .11254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 accgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacgtcgagccg
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/protein_id="AAC63623.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 ctcggcgcctacctccaccgctaccgcgagttcgagggcga 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5%; Score 122.6; DB 1:
64.8%; Pred. No. 2.4e-09;
tive 0; Mismatches 99
                                                                                                                                                    complement(11382...11410)
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                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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SOURCE
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COMMENT

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Lusyotta, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryotta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 266340)

Sadams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Annanatides, D.G., Scherer, S.E., Lip, Pw., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor, Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Markeys-Pfannkoch, C., Barker, E.G., Helt, G., Nelson, C.R., Gabor, Miklos, G.L., Abril, J.F., Bladwin, D., Ballew, R.M., Bason, K.Y., Barcadale, J., Bayraktaroglu, L., Beasley, E.M., Beson, K.Y., Burnan, M.R., Bouck, J., Brokstein, P., Bottler, P., Burtis, K.C., Busam, D.A., Buller, H., Cadleu, E., Center, A., Chandra, I., Cawley, S., Danlike, C., Davenport, L.B., Davies, P., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunnkov, B.C., Downes, M., Dugan-Rocha, S., Dunnkov, B.C., Perriars, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S.,
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Drosophila melanogaster genomic scaffold 142000013386055 section 57
           sequence e-mail to fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 gatotoggacgacgacgaggaggacgatocaggagtgcgtgtcggagtacatcatcat 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23793 TAGCAGTGAGGCCATCGAACGTAGCGTCGCGGAAATCGCAAGACACTCAACGGGACGA 23852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 gctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgacgccaa 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 cgccaacaatggcgcgctgctcagcagcatgcggcgcggcgatccgcgagcaggaccg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
For further information on this sequence e-mail to fly@cel * NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      Length 24766;
                                                                                                                                                                                                                                                                                                                                                    10.4%; Score 12%, 61.2%; Pred. No. 6e-09; Indels +ive 0; Mismatches 125; Indels
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/organism="Drosophila melanogaster"
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5459 c 5043 g
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Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M. L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Mostin, D., Houston, K.A., Howland, T.J., Wei, M. H., Eloywan, C., Jalali, M., Kalush, F., Karpen, G.H., Kee, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lail, Z., Lasi, Y., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Lidang, Y., Lin, X., Mattei, B., McIntosh, T.C., McLeod, M.P., Morberson, D., Merkulov, G., Milshina, N.V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, D., Musskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Pusher, M., Palazzolo, M., Pittman, G.S., Pan, S., Saunders, R.D., Scheeler, F., Shen, H., She, B.C., Siden-Kiamos, I., Stapleton, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapleton, M., Skrong, R., Sun, E., Syirsks, R., Tector, C., Turner, R., Wann, R., Mann, R., Wann, R.,
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2958. .3179,3470. .3591,3725. .>3906))
/gene="CG10462"
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VQIKEEPLNAEEADRMLLEDNPPLNVKLEPQDEEMPDVSRIKEEQSNGSVWTAIHTPL
RNKLRLPALATTKNOMHLKRKFFAINNKSSYIIITTFSAGVKRNGLLTSNVESLNKKS
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DSPTVTLSGTENSTNFIKIPKTISISTVGSMGNPHASAKTVQPTQTHSRSSCFLVDSF
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VLMESKOTSALSNYPVNKGLESPTSINYERPKYKRKRKAGSRCTECLEKVFTTFGAL
RIHKSIHTGELPYQCSYCDKRFRTPGQVRHRRHTGERPFKCKIGSLDFTHRETLIS
HLSRHIGMRYKCYGCDKYFVVVSGLRAHRRLRPDTCGKVKFTARAHGPRVRVIRGEV
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LHFCRLGCGIWLDTLEKILEHEYRQHFQPGRVLCCRVCDFMANSADDLASHMQKHIYV
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Adams, M.D., Celliker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter, E., Wang, A., Wang, X., Wang, Z. Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zhang, L., Zhang, G., Zhao, Q., Zhang, L., Zhang, K. C., Zhao, W., Zhong, W., Zhong, W., Zhong, W., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C. Science 287 (5461), 2185-2195 (2000)
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/db_xref="taxon:7227"
/chromosome="2L"
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complement()oin(542. .567,703.
2958. .3179,3470. .3591,3725. ...
/gene="CG10462"
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/protein_id="AAF53838.1"
/db_xref="GI:7298622"
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/db_xref="FLYBASE:FBgn0032815"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<542. .>3906)
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Location/Qualifiers
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JOURNAL
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AUTHORS
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JOURNAL

TITLE

FEATURES

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YGKIHDNPKNLYVEEKRCCLNFCRRSRSSDFNMSLYRFPRDEVLLRRWCYNLRDDGV
YRGKHRKICSAHFIKEALGILKLSPQAVPTLHIGHTDTFNIYENELWPPPTAPNSHSS
GLQHQTQQRSASGHSLQQQLHSKSYHROSASTSSASSANSHYVDPDLSASYLGIGAS
GSSANMASDSMDVCVPSCESKRHNENITFHTIPRRPEQMRKWCHNIKIPEEKMHKG
MRICSLHFEPYCIGGCMRPFAVPTLNLGHDDDDIHRNPDVIKKLNIRETCCVAVCKRN
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EVNTKMERSYSNSTGESSYSYODSGYNNAYGSDSSMIAGAIAGPQAHSSTLDDSEDAL
CCVPLCGVRKSTSPTLQFTFVDEWTKINQMLHNLKMFHIPAASYANFRICSMHFPKR
CINRYSLCYMANPTPRHGADDVANLYQNRELTNTFTTGEVARCSMPHCTSQRGSBNLK
FYNFPKDIKSLLYMANPTHOODVANLYQNRELTNTFTTGEVARCSMPHCTSQRGSBNLK
FYNFPKDIKSLIKWCQNARLPVQAKEPRHFCSRHFEERCIGKFRLKFWAVPTLHLGAQ
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AVPTLSLGHENIPYPLPTPEQVTEFYSRPTAPNNGEEGGECCVETCKRNPSVDDIKLY
RPPEEASVLAKWAHNLQTESSQLTSMRICNLHFEAHCIGKRMRPWAIPTLNLAGTIEN
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RVCSRHFETHSFUGRRLSAGAIPTLELGHDDEDIYPNEAQAFADEHCVVEGCEASKEQ
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LVETPAEHPSDDEAEYRGDEEDERDEDEDLDEAEHFHPDNPPTPPTIPLRREKPANNV
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EPIDEHSYKSNYIDDNTPFADFSKFSEFSEDMLSPKVELTVKDESYGRTTSSFLERRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLAKWAHNLQVPMVGSAQRRLCSAHFEPHVLSKKCPVPLAVPTLDLNAPPGLKIYQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELGHDDADIELVLNPKPEDRYVDPVFKCIVPTCGKTRRFDEVQMNSFPKDANLFERWK
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RESULT 14
AC007063 82403 bp DNA PLN 05-APR-2000
DEFINITION Arabidopsis thallana chromosome II section 76 of 255 of the complete sequence. Sequence from clones T10F5, F13J11.
AC007063 AE002093
VERSION AC007063.5 G1:6598657
HTG. Cress.
HTG. Cress.
ORGANISM Arabidopsis thallana Enhryophyta; Tracheophyta; Spermatophyta; Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Brassicales; Brassicaeae; Arabidopsis.

REFERENCE I (bases 1 to 82403)
Lin, X., Kaull,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Feldblyum,T.V., Bueil,C.R., Ketchum,R.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,

Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:4558656. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html). Sequence and analysis of chromosome 2 of the plant Arabidopsis Nature 402 (6763), 761-768 (1999) (bases 1 to 82403) Direct Submission Venter, J.C thaliana 20083487 Lin, X AUTHORS JOURNAL JOURNAL PUBMED REFERENCE TITLE COMMENT

genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gromic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named similarity to other proteins are named similarity but with EST similarity to other proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are predicted by tRRAscan-SE (Sean Eddy, Simple repeats were http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/kM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Exic Richhards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org. Location/Qualifiers /note="Sequence from clone T10F5' /organism="Arabidopsis thaliana" complement(7998. .11670) /gene="At2g13470" .3308) 1197. .1306 /rpt\_family="(TAAAA)n" complement(3226. .3308) /rpt\_family="(TAAAA)n" 7744. .7865 /rpt\_family="(TAAAA)n" /cultivar="Columbia" /db\_xref="taxon:3702" /chromosome="II" /note="T10F5.1" 1.82403.82202 repeat\_region repeat\_region repeat\_region misc\_feature gene FEATURES

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ATHAP3A
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                                                                                                                                                                                                                                                                                                                                                                                                                            KEKQTARDMIYWIEETIIYPYHGFEYTLIVYQTLLDIGSKSTTHLYYVLERYGOVFSK
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EGEPVLGENPAMKRLKSTVEKTGEAELSLRESLEAKEALNRALSETEVLYISLMQH
MILLFPFIY
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RALFEKISDLDMESRTRLILWFSHHLSNFQFIWPWEEWAFVLDLPKWAPKRVFVQEIL
QREVRLSYWDKIKQSIENATALEELLPPRAGPNFMYSLEEGKEKTEEQQLSAELSRKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46631 AATGGAGATGATATCATTTGGGCTATCACAACTCTCGGTTTCGAAGACTACGTGGCTCCA 46572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46691 ATTAGTTTCGTCACTGGTGAAGCTTCTGACAAGTGTCAAAGAGAAAAGAGGAAGACCATC 46632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46811 GAACAAGACCGGTTTCTTCCCATTGCGAATGTCGGAAGGATCATGAAAAAAAGTTCTTCCC 46752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 accgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacgtcgagccg 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 gogcacgecaagateteggacgacgecaaggagacgatecaggagtgegtgteggagtae 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(<40516. 40686,40766. 40862,40943. 41061,41171
41499. 41627,41718. 41778,42210. 42313,42390. 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 gagcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcggcgtgctgccg 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATHAP3A 832 bp mRNA PLN 12-SEP-1997
Arabidopsis thaliana mRNA for Hap3a transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46571 TTAAAGGTCTACCTCTGCAAATATAGAGACACCGAAGGAGA 46531
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Barssicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 832)

Edwards,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xxef-"SPTREMEL:023633"
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132 c 204 g 244 t
                                                                                                                  Direct Submission
Submitted (12-JUN-1997) Edwards D., Plant Sciences, University of
Submitted, Downing Street, Cambridge CB2 3EA UK
2 (bases 1 to 832)
Edwards, D., Smith, A.G. and Murray, J.A.
Isolation and characterisation of CCAAT box binding proteins from
Unpublished
                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .832
/ organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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103. .528
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ORIGIN
                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                 JOURNAL
FEATURES
                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                              gene
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ö 0; Gaps Query Match 9.1%; Score 107; DB 13; Length 832; Best Local Similarity 61.1%; Pred. No. 3.8e-06; Matches 173; Conservative 0; Mismatches 110; Indels ò

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295 acatcagcttcatcacgggggggggccaacgagcggtgccagcgggagcagcgcaagacca 354 δŏ q ò

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Search completed: October 25, 2001, 12:05:47 Job time: 4682 sec

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October 25, 2001, 09:19:30 ; Search time 12.26 Seconds (without alignments) 466.894 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                             US-09-435-054-2
1514
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Perfect score:
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                                                                                                                 Run on:
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197339 Total number of hits satisfying chosen parameters:

197339 seqs, 20590346 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_patents\_AA:\*
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5: /cgn2\_6/ptodata/2/iaa/FB\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/FCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Segmence	Secuences	Seguences	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Secretary	Seguence	Souther	Sequence	Seguence	Segmence	Source Person	Seguence	Sections	Sourches	Sequence	Sequence	Sequence	
SUMMARIES	ID	US-09-103-478-2	US-09-103-478-19	US-09-103-478-20	US-09-103-478-22	US-09-103-478-21	US-09-103-478-24	US-09-103-478-25	US-09-103-478-26	US-09-319-989-4	US-09-103-478-28	US-09-103-478-27	US-09-103-478-29	US-09-103-478-23	US-08-681-812-7	US-09-041-886-23	US-08-845-998-8	US-09-206-537-8	US-09-041-886-11	US-07-945-283-2	US-08-864-038A-3	US-09-010-928B-4	US-09-431-573-5	US-09-083-351-2	US-09-083-352-2	US-09-010-928B-28	US-09-010-928B-2	US-09-431-573-4	
	DB	4	4	4	4	4	4	4	4	4	4	4	4	4	-	4	7	4	4	П	~	7	4	m	4	~	7	4	
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	Result No.	1	7	m	4	in v	ıΩ	~ `	ж (	э <b>л</b> (	01	Π;	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	2.1	

Sequence 5, Appli Sequence 7, Appli	Sequence 13, Appl Sequence 15, Appl Sequence 80, Appl Sequence 80, Appl	45, 51, 2,	Sequence 1, Appli Sequence 1, Appli Sequence 18, Appl Sequence 16, Appl	Sequence 16, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 4, Appli
US-08-123-343A-5 US-08-123-343A-7 PCT-US96-02331-13	PCT-US96-0231-15 US-08-477-509B-80 US-08-482-085B-80	US-08-175-155-45 US-08-707-237A-51 US-08-712-948-2	US-08-712-948-1 US-08-931-820-1 US-08-963-825-18 US-09-121-321-16	US-08-933-803A-16 US-07-609-716-36 US-08-475-411A-36 US-08-478-029A-36 US-08-425-069-4
7 7 7	3 1 2	- 777	~~~~	41441
410 410 340	842 2100 2100	2107 2107 330	333 1057 1341 671	671 1038 1038 1038 595
7.17.17.0	7.0	0.0.9	0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
107 107 106	105.5 105.5	105.5	103.5 103.5 103	103 103 103 103
28 29 30	33.2	9 8 8 8 4 8 9 1	38 39 40 1	4 4 4 4 1 2 6 4 4 5 4 6 8

## ALIGNMENTS

	; MOLECULE TYPE: protein US-09-103-478-2
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US-09-103-478-19

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68 YISFVTGEANERCOREORKTITAEDILWAMSKLGFDNYVDPLTVFINRYREIETD-RGSA 126
                                                                                                                                                                                                                                                                            136 LVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHDMQMHAAMYGGTAVPPP 195
                                                                                                                                                                                                                                                                                                                       76 YISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                                    196 AGPPHHGGFLMPHPQGSSHYL----PYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSG 251
                                                                                                                                                                                                                                                                                                                                                                                                               144 -----GF----HGPSHGLPPPGPYGY----GMLDQSMVMGGGRYYQ-NGSSGQDES 185
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                                                                                                                  32.6%; Score 494; DB 4; Length 208; 47.0%; Pred, No. 2.3e-38; Live 19; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lottan, Tamar
APPLICANT: Obto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Foldberg, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PACHOES/MS-DOS
SOFTWARE: Pachentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/POCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/103,478 FILING DATE: 24-JUN-1998 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09103478 Patent No. 6235975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 90 amino acids amino acid
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       Query Match 32.6%
Best Local Similarity 47.0%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarcade CITY: San Francisco STATE: Calofornia COUNTRY: USA ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                             0; Gaps
                                                                                                                                                                                                                                36 REQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Manar
APPLICANT: Ohto, Mas and a Rabin a Rabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.5%; Score 341; DB 4; Length 90; 65.6%; Pred. No. 1.1e-24; tive 19; Mismatches 12; Indels
Query Match 26.6%; Score 403; DB 4; Length 90; Best Local Similarity 82.2%; Pred. No. 2e-30; Matches 74; Conservative 11; Mismatches 5; Indels
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SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                   96 ITAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
                                                                                                                                                                                                                                                                                                                                                                                                                      61 ITAEDILWAMSKLGFQNYVDPLTVFINRYR 90
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FILING DATE: 24-JUN-1998
CLASSIFECATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 20, Application US/09103478
; Patent No. 6235975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
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Matches 59; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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1 REQDRFLPIANISRIMKKAIPANGKIAKDAKETVQECVSEFISFITSEASDKCQREKRKT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Lotan, Tamar
APPLICANT: Oldo, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.1%; Score 305; DB 4; Length 90; Best Local Similarity 64.4%; Pred. No. 2.3e-21; Matches 58; Conservative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IEBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-70N-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTONREY/AGERT INFORMATION:
NAME: C. ADAMONTONE
                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
                                       96 ITAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
                                                               96 ITAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/09103478
Patent No. 6235975
GENERAL INFORMATION:
APPLICANT: Harada, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ 1D NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 576-0200
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-103-478-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calofornia
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94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                        US-09-103-478-22
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US-09-103-478-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/09103478
Patent No. 6235975
GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Ohto, Masa-ak,
APPLICANT: Ohto, Masa-ak,
APPLICANT: Gidberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Obloo, Masa-aki
APPLICANT: Obloo, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.9%; Score 301; DB 4; Length 90; 63.3%; Pred. No. 5.5e-21; tive 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                   STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: Calofornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
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APPLICATION NUMBER:
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 24, Application US/09103478 ; Patent No. 6235975
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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Matches 57; Conserv
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PRIOR APPLICATION DATA:
MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Lotan, Tamar
APPLICANT: Olto, Mass-aki
APPLICANT: Glodbert B.
APPLICANT: Glodbert B.
APPLICANT: Fischer, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert B.
APPLICANT: Fischer, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: SEQUENCES: 29
CORRESPONDENCE ADDRESS: 39
CORRESPONDENCE ADDRESS: 39
CORRESPONDENCE ADDRESS: 400 Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: Calofornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.3%; Pred. No. 5.5e-21;
Matches 57; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                       SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/103,478 FILING DATE: 24-JUN-1998 CLASSIFICATION: 800
                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                       ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: EINDER, Gregory P.
REGISTRATION NUMBER: 38,440
REFENDE/COCKET NUMBER: 023070-077611US
TELEPHONE: (415) 576-0200
TELEPAN: (415) 576-0300
INPORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 ITAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 INGEDILFAMSTLGFQSYVEPLKLYLQKFR 90
                                                                                                                                                                                                                                                                                                                                                                                                    PROOF APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-103-478-25; Sequence 25, Application US/09103478; Patient No. 6235975; EBNERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-103-478-24
            NUMBER OF SEQUENCES: 29
                                                                                                                             Calofornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                             STATE:
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36 REQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Loto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer. Leafy COTYLEDONI Genes and Their Uses
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.9%, Score 301; DB 4; Length 90; 63.3%; Pred. No. 5.5e-21; tive 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                   NAME: Einhorn, Gregory P.
RECISTRATION NUMBER: 38,440
REFERENCE/DOKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 ITAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
                                                                                                         APPLICATION NUMBER: US/09/103,478 FILING DATE: 24-JUN-1998 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                              US 08/804,534
            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
Floppy disk
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Best Local Similarity 63.3%
Matches 57; Conservative
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LENGTH: 90 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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ZTP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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36 REQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKT 95
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APPLICANT: Lotan, Tamar
APPLICANT: Lotan, Tamar
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
ATTLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 17.8%; Score 270; DB 4; Length 90; 1 Similarity 56.7%; Pred. No. 4e-18; 51; Conservative 16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two Embarcadero Center, Eighth Floor
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APPLICATION NUMBER:
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | ||:| :: |||::| | || :|| 61 INGEDILISLHALGFENYAEVLKIYLAKYR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/103,478 FILING DATE: 24-JUN-1998 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        ; Sequence 28, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 27, Application US/09103478; Patent No. 6235975; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elnhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28.
SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: peptide
US-09-103-478-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: Calof
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STREET: TV
                                                                                                                                                                        US-09-103-478-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-103-478-27
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APPLICANT: Grivell, Leslie A.
APPLICANT: Grivell, Leslie A.
APPLICANT: Grivell, Leslie A.
APPLICANT: Grivell, Leslie A.
APPLICANT: Blom, Jolanda
TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: ME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYRE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.7%; Score 298; DB 4; Length 90; 61.1%; Pred. No. 1e-20; tive 19; Mismatches 16; Indels
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US-09-319-989-4
                                                                                                                                                  TORNEY/AGENT INFORMANCE BITHOUR, Gregory P.
REGISTRATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 ITAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
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                      FILING DATE: 19-FBB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FBB-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09319989
Patent No. 6190914
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Best Local Similarity 61.18
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-103-478-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Matches 60; Conserva
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US-09-319-989-4
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LENGTH: 144
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Two Embarcadero Center, Eighth Floor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-103-478-29
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Calofornia
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                                                                                    94111-3834
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                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Obto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0%; Pred. No. 4.6e-18;
Matches 51; Conservative 18; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: Calofornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFRENCE/COCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 27:
SEQUIENCE CHARACTERISTICS:
LENGTH: 85 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION UNDERF: US 09/026,221
FILING DATE: 19-FEB-1998
PHIOR APPLICATION DATA:
APPLICATION UNDERF: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
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US-09-103-478-29
; Sequence 29, Application US/09103478
; Patent No. 6235975
; GRNERAL INFORMATION:
APPLICANT: Harada, John
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MOLECULE TYPE: peptide
US-09-103-478-27
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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37 EQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKTI 96
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APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Mass and
APPLICANT: Ohto, Wass and
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Rober
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                                                                            PatentIn Release #1.0, Version #1.30
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Einhorn, Gregory P.
REGISTRATUN NUMBER: 38,440
REFERENCE/DOKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPACK: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 TAEDVLWAMSRLGFDDYVEPLGAYLHRYR 125
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                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PULDA STATEMENT OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-103-478-23
; Sequence 23, Application US/09103478
; Patent No. 6215975
; GENERAL INFORMATION:
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0; Gaps

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US-09-041-886-23
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                                                                                                           US-08-681-812-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TBP-Associated Global Negative Regulator TITLE OF INVENTION: and Methods of Use Thereof NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 208; DB 4; Length 57; 66.7%; Pred. No. 1.2e-12; tive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/681,812
FILING DATE: 29-JUL-1996
CLASSIFICATION: A35
                                                                                                                                                                                                                                                                            023070-077611US
                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY AGENT INFORMATION:
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,478
FILING DATE: 2-UN-1998
CLASSIFICATION: 800
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                                                                                                                                                                                                                          NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SED ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08681812
Patent No. 5763593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHIST
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Young, Richard A. APPLICANT: Gadbois, Ellen L. APPLICANT: Chao, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.79
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : MOLECULE TYPE: peptide US-09-103-478-23
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                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 HPHSMSPA--AMLKSRGPVSGAAMLPHHHHHHDMQMHAAM-----YGGTAVPPPAGPPH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 HGGFLMPHPQGSSHYL-PYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSGSGGGG--- 256
                                                                                                                                                                                                                                                                                  56; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.7%; Score 147; DB 4; Length 1185;
31.7%; Pred. No. 2.7e-05;
tive 11; Mismatches 56; Indels 3
                                                                                                                                                                                Length 156;
                                                                                                                                                                                                                                                                                                                                          97 TAEDVLWAMSRIGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAAPSR 144
                                                                                                                                                                                                                                                                                                                                                                     63 SPEHVIQALESLGF-----GSYISEVKEVLQECKTVALKRKASSR 103
                                                                                                                                                                                                                      38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                   Query Match

10.6%; Score 160; DB 1;
Best Local Similarity 31.5%; Pred. No. 1.2e-07;
Matches 34; Conservative 28; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09041886
Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        = :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4370 La Jolla Vil
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (619) 535-9001
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1185 amino acids
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                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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- 513 -----PLEGGSSHHAHPYAMSPSLG---SLRPYPPGPAHLPPPHSQVSYSQAGPNGPPV 563 qq
- Ω
  - qq

Search completed: October 25, 2001, 09:21:43 Job time: 133 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 25, 2001, 09:16:40; Search time 20.67 Seconds (without alignments) 815.359 Million cell updates/sec Run on:

US-09-435-054-2 1514 Title: Perfect score:

1 MDSSSFLPAAGAENGSAAGG.....ASHTPQGSGGLEHPHPFAYK 278 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

412676 seqs, 60623988 residues Searched:

Total number of hits satisfying chosen parameters:

412676

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/ SIDSB/990data/geneseq/geneseqp/AA1980.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1990.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1991.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1992.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1992.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1995.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1995.DAT:\*
/ SIDSB/990data/geneseq/geneseqp/AA1995.DAT:\*
/ SIDSB/990data/geneseqf/geneseqp/AA1995.DAT:\*
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/ SIDSB/990data/geneseqf/geneseqp/AA1999.DAT:\*
/ SIDSB/990data/geneseqf/geneseqp/AA1999.DAT:\* /SID88/gcgdata/geneseq/geneseqp/AA1980. DAT: \*
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/SID88/gcgdata/geneseqp/AA1983. DAT: \*
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/SID88/gcgdata/geneseqp/AA1983. DAT: \*
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/SID88/gcgdata/geneseqp/AA1985. DAT: \*
/SID88/gcgdata/geneseqp/AA1986. DAT: \*
/SID88/gcgdata/geneseqp/AA1987. DAT: \*
/SID88/gcgdata/geneseqp/AA1988. DAT: \*
/SID88/gcgdata/geneseqp/AA1988. DAT: \* A\_Geneseq\_0601:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Maize LECI # 1. 2 Soybean LECI # 2 p Soybean LECI # 1. Arabidopais leafy Anno acid sequenc Wheat LECI. Triti Veronia mespilifol Argemone mexicana Soybean LECI # 3. Pinus radiata tran	
SUMMARIES	ID	AAY96214 AAY96220 AAY96216 AAY96216 AAY96216 AAY96217 AAY96217 AAY96217 AAY96217 AAY96217	
	DB	21 21 21 21 21 21 21 21 21 21	
	Query Match Length DB	278 355 373 373 240 208 208 280 214 . 146	
ф	Query	1000 3401 3411 3216 3216 3216 3213 3210 22913 22913	
	Score	1514 516.5 516.5 16.5 608 4994 48999 484 4444 443	
	Result No.	1 2 3 4 4 4 7 7 7 10 11	

4,44,4	# 3. # 3. s thal ata tr grand ata tr	thali thali consen grandi ta tra grandi	Arabidopsis Unital Arabidopsis thalia Maize LECI # 2 Z Arabidopsis thalia Arabidopsis thalia Human C-Maf protei Arabidopsis thalia Pinus radiata tran	ote ote ote th th th tin
AAY96225 AAG04651 AAG31928 AAG49286 AAR15481	AAY96 AAG04 AAB33 AAB33 AAB33		AAC08106 AAY96218 AAG45969 AAX31232 AAC08108 AAB33004	
				93 21 96 21 98 20 153 21 138 21 186 22 113 20 1185 20
7 4 E E H H	000000	15.0 14.9 13.2 13.1	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	11.3 11.3 11.3 11.2 10.9 9.7
409 376.5 360.5 360.5 324.5		287 235 226 200 199 197	197 192 185.5 185.5 182.5 173	1/1 1/1 1/1 1/1 169.5 165.5 147 144
12 13 14 15 16	18 19 20 22 23	22 22 23 24 29	30 33 33 30 30 30 30	888 938 938 94444 95 95 95

## ALIGNMENTS

AAYY	0
	AMISOZI4 SLAMUATU; Procein; 2/8 AA.
	AAY96214;
	11-SEP-2000 (first entry)
	Maize LEC1 # 1.
	Maize; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
	screetarte mainei, transgenic plant; transgenic seed; HAP3.
	2ea mays.
	WO200028058-A2.
	18-MAY-2000.
	09-NOV-1999; 99WO-US26514.
	09-NOV-1998; 98US-0107643. 10-NOV-1998; 98US-0107810.
	(PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.
	Lowe KS, Gordon-Kamm WJ, Klein TW, Rasco-Gaunt S, Cahoon RE; Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
	WPI; 2000-376568/32. N-PSDB; AAA27450.
	New HAP3-type CCAAT-box binding transcriptional activators.

New HAP3-type CCAAT-box binding transcriptional activators,

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0
                                                                               The present sequence is the maize leafy cotyledon 1 transcriptional activator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the nucleilus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1 transpenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 isddaketigecvseylsfitgeanercqreqrktitaedvlwamsrlgfddyveplgay 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LHRYREFEGDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHDM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 QMHAAMYGGTAVPPPAGPPHHGGFLMPHPQGSSHYLPYAYEPTYGGEHAMAAYYGGAAYA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ISDDAKETIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDSSSFLPAAGAENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAK 60
 useful for
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                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1514; DB 21; Length 278; 100.0%; Pred. No. 3.3e-127; 1.1ve 0; Mismatches 0; Indels 0;
particularly Leafy cotyledon 1 transcriptional activator, u
inducing somatic embryogenesis or apomixis in a plant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 PGNGGSGDGSGSGGGGGSASHTPQGSGGLEHPHPFAYK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                         Claim 13; Page 77-78; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96224 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soybean LEC1 # 2 protein # 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107810.
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0
Best Local Similarity 100.0
Matches 278; Conservative
                                                                                                                                                                                                                                                                                                                              278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200028058-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1998;
10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96224;
                                                                                                                                                                                                                                                                                                                              Seguence
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the present sequence is a HAP3-type CCAAT-box binding protein. Cartivator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein. EC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When appmixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, c.e. the megaspore mother cell would trigger embryo formation from anternal tissues only. This results in the production of seeds identical to the parent Using LEC1, transgenic high yielding seeds could be concluded. The addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.

Note: this sequence is different from that of AAY36220, ewen though they are both encoded by the same nucleotide sequence (AAAZ7460). The AAY36220 sequence has 18 stop codons distributed throughout the CDS, while the protein of AAY36224 has the stop codons comitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 YISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 LVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHHHHDMQMHAAMYGGTAV--- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                                                                                                                                                                                                          present sequence is the soybean leafy cotyledon 1 transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 SAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: :| || : :| || 38 ssdgncsnhsaageenectvreqdrfmplanvirimrkllpphakisddaketiqecvse 97
                                                                                                                  New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..373
/note= "All Xs are unspecified residues encoded by stop codons"
  Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.1%; Score 516.5; DB 21; Length 355; 53.8%; Pred. No. 3.3e-38; tive 16; Mismatches 50; Indels 31;
Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S,
Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 PPPAGPPHHGGFLMPHPQGSSHYLPYAYEP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 ppnaasshh-----hhgisnahep 219
                                                                                                                                                                                                         Claim 13; Page 89-90; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96220 standard; Protein; 373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean LEC1 # 2 protein # 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity 53.8%
                                                               WPI; 2000-376568/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 1.
                                                                                      N-PSDB; AAA27460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Query Match 33.6%
Best Local Similarity 52.5%
Matches 114; Conservative
                                                                                                                                                                                                                                                            , Gordon-Kamm
Hoerster GJ,
                                                                                                                                                                                                                                                                                                    WPI; 2000-376568/32.
N-PSDB; AAA27456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA;
     Soybean LEC1 # 1.
                                                                                               WO200028058-A2.
                                                                                                                                                     09-NOV-1999;
                                                                                                                                                                                09-NOV-1998;
                                                                                                                                                                                            .0-NOV-1998;
                                                                       Glycine max
                                                                                                                         18-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW71722;
                                                                                                                                                                                                                                                            Lowe KS,
                                                                                                                                                                                                                                                                          Sun X,
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                                                                                                                                                                                                                                                                                                                   The present sequence is the soybean leafy cotyledon I transcriptional activator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the nucleilus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be ceveloped. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.

Note: this sequence is different from that of AAY96224, even though they are both encoded by the same nucleotide sequence (AAA27460). The AAY96220 sequence has 18 stop codons distributed throughout the CDS, while the protein of AAY96224 has the stop codons omitted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 YISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHDMQMHAAMYGGTAV--- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: :| || : :| || 38 ssdgncsnhsaageenectvreqdrfmpianvirimrkilpphakisddaketiqecvse 97
                                                                                                                                                                                                                                                       particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSE 75
                                                                                                                                                               Rasco-Gaunt S, Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 34.1%; Score 516.5; DB 21; Length 373; al Similarity 53.8%; Pred. No. 3.5e-38; 113; Conservative 16; Mismatches 50; Indels 31;
                                                                                                                                                                                                                                          New HAP3-type CCAAT-box binding transcriptional activators,
                                                                                                                                                                           Gregory CA, Nadimpalli R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 PPPAGPPHHGGFLMPHPQGSSHYLPYAYEP 222
                                                                                                                                                               Gordon-Kamm WJ, Klein TM,
                                                                                                                  (PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                               Claim 13; Page 89-90; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96216 standard; Protein; 240 AA
                                                                              98US-0107643.
98US-0107810.
                                                      99WO-US26514
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                                                                                                                                                                          Hoerster GJ,
                                                                                                                                                                                                   WPI; 2000-376568/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 AA;
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WO200028058-A2
                                                   09-NOV-1999;
                                                                                          10-NOV-1998;
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                          18-MAY-2000
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                                                                                                                                                             Lowe KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                           Sun X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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The present sequence is the soybean leafy cotyledon 1 transcriptional activator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein. LEC1 expression intitates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the nuclellus integument, or cell specific expression in the magaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.
Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 DARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHHDMQMHAAMYGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 QECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 drtsm----rgeplgkrtveyatl----gvatafvpppyhhngyfgaampmg 202
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52.5%; Pred. No. 1.2e-37;
.ive 19; Mismatches 52; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::: :| | | ::: .| | 47 assdhsaatgeene-----ctvreqdrfmpianvirimrkilpphakisddaketi 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly Leafy cotyledon l'transcriptional activator, useful for
inducing somatic embryogenesis or apomixis in a plant cell ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
Gregory CA, Nadimpalli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New HAP3-type CCAAT-box binding transcriptional activators,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 tyvreappntasshhhhhhhhhargisn---ahep 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
(DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 82; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107810.
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(first entry)

252 SGGGGGSAS 260

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEC1 polypeptide is encoded by the leafy cotyledon-1 (LEC1) gene (see AAV61022-24) of Arabidopsis thaliana. Full-length LEC1 polypeptide can act as a subunit of a protein capable of acting as a transcription factor in plant cells. The LEC1 gene is embryo-specific and can be used to modulate development (claimed) of embryos or other organs in plants. Inhibiting expression can be useful e.g. in weed control (by transferring an inhibitory sequence to a weedy species and allowing it to be transmitted through sexual crosses) or to produce fruit with samil and non-viable seed. Enhanced expression of LEC1 can be used to increase storage protein content in plant tissues to improve nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 YISPITGEANERCOREORKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 LVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHHDMQMHAAMYGGTAVPPP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 AGPPHHGGFLMPHPQGSSHYL----PYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated plant leafy cotyledon-1 gene - used to develop products for, e.g. increasing storage protein content in plant tissues, or producing fruit with small and non-viable seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 SAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 agagdknngivvqqqppcvareqdqympianvirimrktlpshakisddaketiqecvse 67
                                                                                                                                                                                                                                           /note= "putative subunit interaction domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohto M;
                                                                                 LEC1; leafy-cotyledon 1; embryo; transcription factor;
                                                                                                                                                                                                       /note= "putative DNA binding site"
61..72
                                               Arabidopsis leafy-cotyledon 1 (LEC1) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 494; DB 19;
47.0%; Pred. No. 1.7e-36;
tive 19; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lotan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 l----rg----eppslrqt-----
                                                                                                                                    Arabidopsis thaliana ecotype Wassilewskija.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harada JJ,
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 31; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                               98US-0804534.
97US-0804534.
                                                                                                                                                                                                                                                                                                                                              98WO-US02998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldberg RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 47.09
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-531499/45.
N-PSDB; AAV61022-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 AA;
                                                                                                     transgenic plant.
                                                                                                                                                                                      Binding-site
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                                                                                                                                                                                                                                                                                                                                              20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1998;
                                                                                                                                                                                                                                                                                                            27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fischer RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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The present sequence represents a Leafy Cotyledon 1 (LEC1) polypeptide. LEC1 genes are thought to play a central role in late embryogenesis, in specifying cotyledon identity during embryo development. LEC1 polypeptides may act as transcription factors. LEC1 polynucleotides are useful for modulating seed development and for inducing ecotopic development of embryonic tissue in a plant. In both cases, the LEC1 polynucleotide is introduced into the plant through a sexual cross and is co-expressed in a natisense orientation with a second heterologous polynucleotide selected from AP2 and RAP2 genes of Arabidopsis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LECT polynucleotide is also useful for targeting expression in a seed, and for preparing expression cassettes for suppression to enhancing endogenous LECT gene expression, which is useful in weed control or for improving nutritional value of plant tissue respectively. LECT polypeptides and polynucleotides are especially used for increasing or decreasing storage protein content in cotyledons or leaves. LECT also increases reproductive tissue mass, e.g., increases fruit size, seed mass, its protein or its oil.
                                                                                                                                                                                                                                      Leafy cotyledon 1 gene; LEC1 gene; embryogenesis; cotyledon identity; embryo development; transcription factor; seed development; ecotopic development; embryonic plant tissue; weed control; nutritional value; storage protein; cotyledon; seed; reproductive tissue mass; fruit size; seed mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 YISFITGEANERCQREQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of an Arabidopsis leafy cotyledon 1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New embryo-specific gene useful for producing transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fischer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 494; DB 21;
Pred. No. 1.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldberg RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 53-54; 69pp; English.
                                                                                          AAY54563 standard; Protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.6%;
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98US-0193931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lotan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-160588/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 117; Conserva
 186 svgggssss 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        W09967405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1999;
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17-NOV-1998;
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                                                                                                                                AAY54563;
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Gaps

92; Indels

Matches 119; Conservative 27; Mismatches

71 ECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFE-- 128 

58 129

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δy a õ Db δλ g

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11 GAENGSAAGGANNGGAAÒQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQ 70 

AAY96217 standard; Protein; 214 AA.

AAY96217

(first entry)

11-SEP-2000

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Veronia mespilifolia LEC1.

-----GDARGVGLVPGAAPSRGGDHHPHSM-----SPAAMLKSRGPVSGAAMLPH 173

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The present sequence is the wheat leafy cotyledon 1 transcriptional activator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. expression in the nuclellus integument, or cell specific expression in the nuclellus integument, or cell specific expression in the muchallus integument, or cell specific expression in the magaspore mother cell would trigger embryo formation from maternal parent. Using LEC1, transgenic high yielding seeds identical to the addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.
136 LVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLРНННННЭWQMHAAMYGGTAVPPP 195
                                                                          14 -----gf-----hgpshglpppgpyyy----gmldqsmvmgggryyq-ngssgqdes 185
                                                                                                        196 AGPPHHGGFLMPHPQGSSHYL----PYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -
                                                                                                                                                                                                                                                                                                                                                                                                             Wheat; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New HAP3-type CCAAT-box binding transcriptional activators,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rasco-Gaunt S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nadimpalli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon-Kamm WJ, Klein TM,
                                                                                                                                                                                                                                                                                 AAY96222 standard; Protein; 280 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 93; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-376568/32.
                                                                                                                                                                       252 SGGGGGSAS 260
                                                                                                                                                                                                     186 svgggssss 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                              Wheat LEC1
                                                                                                                                                                                                                                                                                                                 AAY96222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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Leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.

Veronia mespilifolia.

WO200028058-A2.

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The present sequence is the leafy cotyledon I transcriptional activator, LEC1 of Veronia mespilifolia. This sequence is a HAP3-type CCAAT-box bidding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. During abomixis, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the nuclellus integument, or cell specific expression in the megaspore mother cell triggers embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing
                                                                                                                                                                                                                                                                                                                                                                                                   particularly Leafy cotyledon 1 transcriptional activator, useful for
inducing somatic embryogenesis or apomixis in a plant cell
                                                                                                                                                                                                                                                                                                                                                                              New HAP3-type CCAAT-box binding transcriptional activators,
                                                                                                                                                                                                                                                                                           Gregory CA, Nadimpalli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 83-84; 94pp; English.
                                                                                                                                                                                                                                                                                         Hoerster GJ,
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                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA27457.
                                                                                                                                                                                                                                                                                           Sun X,
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DB 21; Length 280;

Score 489.5; DB 2. Pred. No. 6.3e-36;

Query Match Best Local Similarity 41.5%;

Cahoon RE;

Rasco-Gaunt S,

Gordon-Kamm WJ, Klein TM,

Lowe KS,

(PION-) PIONEER HI-BRED INT INC. (DUPO ) DU PONT DE NEMOURS & CO E I.

99WO-US26514. 98US-0107643. 98US-0107810.

09-NOV-1999; 09-NOV-1998;

18-MAY-2000.

10-NOV-1998;

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11-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max.
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                                                                                                                                                                                                                                                                                                                                               AAY96221;
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                                                                                                                                 Seguence
                                                                                                               plants.
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                                                                                                                                                                     82 GEANERCOREORKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAA 141
                                                                                                                                          94 geandrcgregrktitaedvlwamsklgfddylepltvylhryrefdggerg----- 145
                                                                                                                                                           142 PSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHH--HHHDMQMHAAMYGGTAVPPPAGP- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell -
                                                                      Gaps
                                                                                                 transformation efficiency and for increasing recovery of regenerated
                                                                                      22 NNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEXISFIT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cahoon RE;
                                                                     20;
                                                                                                                                                                                                                                                                                                                              Leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                    Length 214;
                                                                     49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WJ, Klein TM, Rasco-Gaunt S,
Gregory CA, Nadimpalli R;
                                                   32.0%; Score 484; DB 21;
56.0%; Pred. No. 1.4e-35;
tive 16; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                    /label = unknown /note = "Encoded by GNA"
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Misc-difference 143
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                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                           AAY96215 standard; Protein; 146 AA.
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98US-0107810.
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                                                           Best Local Similarity 56.0% Matches 108; Conservative
                                                                                                                                                                                                                                                                                              11-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon-Kamm WJ,
                                                                                                                                                                                                                                                                                                                Argemone mexicana LEC1.
                                                                                                                                                                                                199 -PHHGGFLMPHPQ 210
                                                                                                                                                                                                               200 gpavagf-epyag 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376568/32.
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 123
                          214 AA;
                                                                                                                                                                                                                                                                                                                                                          Argemone mexicana
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10-NOV-1998;
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                             Sequence
                                                       Query Match
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The present sequence is the leafy cotyledon 1 transcriptional activator, LEC1 of Argemone mexicana. This sequence is a HAP3-type CCAANT-box binding protein. LEC1 expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. During apomixis, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the muchallus integument, or cell specific expression in the medaspore mother cell triggers embryo formation from maternal Lissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 MRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ANNGGAAQQHAAPAIREQDRLMPIANVIRI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 gggggggggggfhgyqklpksnsagmmlselsnnnnnidvnstctvreqdrympianviri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WJ, Klein TM, Rasco-Gaunt S,
Gregory CA, Nadimpalli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.3%; Score 444; DB 21;
63.3%; Pred. No. 3.2e-32;
tive 10; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 DDYVEPLGAYLHRYREFEG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:||| || ||||||||
|124 deyiepltlylqryrefeg 142
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Best Local Similarity 63.3%
Matches 88; Conservative
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Hoerster GJ, Greg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GAENGSAAGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean LEC1 # 3.
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activator, LEGI. This sequence is a HAP3-type CCAAT-box binding protein. Expression initiates the formation of embryo-like structures and the expression initiates the formation of embryo-like structures and the replacement of accovery of transformants. When apomitis occurs, i.e. the replacement of sexual reproduction by assawal reproduction, LECI the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the addition, LECI could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants.
                            present sequence is the soybean leafy cotyledon 1 transcriptional
*55555555555555
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171 AA; Sequence

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0
                                                                                                                                                91 EQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAAPSRGGDHHP 150
                                                                                                                                                                   Gaps
                                                                         31 AAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEXISFITGEANERCQR 90
                                                                                          ;
0
Ouery Match

29.3%; Score 443; DB 21; Length 171;
Best Local Similarity 71.7%; Pred. No. 4.8e-32;
Matches 86; Conservative 7; Mismatches 27; Indels
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Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeoclic; homeoclomain; homeoclos; homeoclomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB. Pinus radiata transcription factor protein sequence #129. AAB33002 standard; Protein; 219 AA. 25-JAN-2001 (first entry) AAB33002; RESULT 11 AAB33002 ò g 

09-MAR-2000; 2000WO-US06112. 99US-0266513. 11-MAR-1999; 18-AUG-1999; 14-SEP-2000

WO200053724-A2.

(FLET-) FLETCHER CHALLENGE FORESTS LTD. GENE-) GENESIS RES & DEV CORP LTD

Glenn M; Shenk MA, McGrath A, Wood M,

WPI; 2000-579369/54.

New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide

Claim 8; Page 387; 747pp; English.

The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such

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transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mabogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, belix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain cys2H1s2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                  76 YISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135
                                                                                                                                                                                                                                                                                                                                                      136 LVPGAAPSRGGDHHPHSMS---PAAMLKSRGPVSG-----AAMLPHHHHHHDMQMHAAMY 187
                                                                                                                                                                                                                                                                                                                                                                                                                             124 kqgdptpskegnnaingssienpnanaysglnpggynrvqsqslph-----mqqaay 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 GGTAVPPPAGP--PHHGGFLMPHPQGSSHYLPYAYEPTYGGEHAMAAYYGGAAYAPGNGG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----nimgay----nmt 197
                                                                                                                                                                                                                                                                    17 AAGGANNGGAAQQHAAP-AIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSE 75
                                                                                                                                                                                                                                                                                      particularly Leafy cotyledon 1 transcriptional activator, useful for inducing somatic embryogenesis or apomixis in a plant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cahoon RE;
                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                             DB 21; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New HAP3-type CCAAT-box binding transcriptional activators,
                                                                                                                                                                                                                                             71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WJ, Klein TM, Rasco-Gaunt S,
Gregory CA, Nadimpalli R;
                                                                                                                                                                                                        27.8%; Score 420.5; DB 2
39.6%; Pred. No. 6.5e-30;
tive 29; Mismatches 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis LEC1 consensus region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 SGDGSGSGGGGSASHTPQG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 apnssggnssggqqqqqprg 217
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                                                                                                                                                                                                                                      Matches 103; Conservative
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                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                             219 AA;
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                                                                                                                                                             Seguence
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19-JUL-1999;
19-JUL-1999;
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14-JUL-1999;
15-JUL-1999;
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16-JUL-1999;
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29-JUN-1999;
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24-MAY-1999;
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                                   06-MAY-1999
                                                  07-MAY-1999;
                                                             11-MAY-1999
                                                                           14-MAY-1
                                                                                                    L4-MAY-1
The present sequence is the leafy cotyledon 1 transcriptional activator, CC consensus sequence from Arabidopsis. This sequence is a HAP3-type CCAAT-box binding protein. LECI expression initiates the formation of embryo-like structures and improves growth and recovery of transformants. When apomixis occurs, i.e. the replacement of sexual reproduction, LECI expression in the nuclellus reproduction by assexual reproduction. LECI expression in the nuclellus conducting to seeds in the medaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LECI, transgenic high yielding seeds could be developed. In addition, LECI could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants. The present sequence (AAY96223).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                  36 REQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQRKT 95
                                                                                                                                                                                                                                                                                                                               27.0%; Score 409; DB 21; Length 90; 83.3%; Pred. No. 2.4e-29; ive 11; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 757.
                                                                                                                                                                                                                                                                                                                                                                   AAG04651 standard; Protein; 141 AA.
              Example 6; Fig 1; 94pp; English.
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990S-0130891.
990S-0131449.
990S-0132048.
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99US-0123180.
99US-0123548.
99US-0125788.
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.33
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          termination sequence
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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21-APR-1999;
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99US-0144085.
99US-0144086.
99US-0144325.
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99US-0134283
99US-0134218
99US-0134219
99US-0134219
99US-0134221
99US-0134768
99US-0134768
99US-0135124
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99US-0135629
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99US-0139492.
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99US-0145088
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99US-0132486
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PR 22-JUL-1999; 9918: 0115/618.

PR 02-MC-1999; 9918: 0116/618.

PR 03-MC-1999; 9918: 0116/618.

PR 11-MC-1999; 9918: 0116/618.

PR 11-MC-1999; 9918: 0116/618.

PR 12-MC-1999; 9918: 0116/618.

PR 13-MC-1999; 9
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                                                                                                                                                                                                                                                            68 TIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREF 127
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                        8 PAAGAENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKE 67
                                                                                                                                                                                           29;
                                                                                                                                                                         DB 21; Length 141;
                                                                                                                                                                       Query Match 24.9%; Score 376.5; DB 21; Length Best Local Similarity 46.0%; Pred. No. 3.2e-26; Matches 75; Conservative 29; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 38427.
                                                                                                                                                                                                                                                                                      128 EGDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM 170
                                                                                                                                                                                                                                                                                                 AAG31928 standard; Protein; 138 AA.
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9905-0123180.
9905-0123180.
9905-0125788.
9905-0126785.
9905-0127465.
9905-0127465.
9905-0128714.
9905-0129873.
9905-0139077.
9905-0130619.
        990S - 0160770
990S - 0160770
990S - 0160815
990S - 0160980
990S - 0160980
990S - 0161405
990S - 0161405
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 990S-0160768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      termination sequence
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
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                                                                                                                                                                                            23.8%; Score 360.5; DB 21; Length 138;
45.4%; Pred. No. 8.3e-25;
ive 29; Mismatches 29; Indels 31; Gaps
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99US-0123180.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 25, 2001, 09:20:20 ; Search time 16.39 Seconds (without alignments) 1292.039 Million cell updates/sec Run on:

US-09-435-054-2

1 MDSSSFLPAAGAENGSAAGG......ASHTPQGSGGLEHPHPFAYK 278 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

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## ALIGNMENTS

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RESULT G86352	protein

- Arabidopsis thaliana prote

C;Species: Arabidopsis thaliana (mouse ear cress) C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C. Jacke: U.Z. Mar. 2001
C. Jacke: U.Z. M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Mathors: Hunter, J.L.; Jackins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia A.; Matthors: Salzaberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Eraser, C.M.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.; Status: preliminary
A.; Status: preliminary
A.; Status: preliminary
A.; Secsiones: 1208 cs70>
A.; Cross-references: GB: AEO05172; NID: 96552738; PIDN: AAF16537.1; GSPDB: GN00141
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.'6									
Ouery Match 32.6%; Score 494; DB 2; Length 208; Best Local Similarity 47.0%; Pred. No. 3.2e-29; Matches 117; Conservative 19; Mismatches 47; Indels 66; Gaps 9;	16 SAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSE 75	:	76 YISFITGEANERCQREORKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVG 135	68 YISFVTGEANERCQREQRKTITAEDILWAMSKLGFDNYVDPLTVFINRYREIETD-RGSA 126	136 LVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLРННННННЭМОМНААМУGGTAVPPP 195	127 LRGEPPSLRQT	AGPPHHGGFLMPHPQGSSHYLPYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSG 251	144GRILPPPGPYGYGMLDQSWVMGGGRYYQ-NGSSGQDES 185	NS 260
ch 11 Simila 117; Co	SAAGGANN	GAGDKNN	ISFITGE	ISFVIGE	VPGAAPSI		GPPHHGGE	GE	252 SGGGGGSAS 260
Query Match Best Local Matches 11	16 Si	. ¥	76 Y	68 Y	136 LV	127 L	196 AG	144	252 SC
Õää	Qy	qq	δy	qq	οy	qq	Qy	QQ	Qy

186 SVGGGSSSS 194

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S22820
R; Li, X.Y.; MantCvani, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis,
Nucleic Acids Res. 20, 1087-1091, 1992
Nucleic Acids Res. 20, 1087-1091, 1992
A; Fitle: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.
A; Reference number: S22816; MUID: 92195809
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C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: A84788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-178 <STO>
A;Cross-references: GB:AE002093; NID:g4371295; PIDN:AAD18153.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Zea mays (maize)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 AKETIQECVSEYISFITGEANERCQREORKTITAEDVLWAMSRLGFDDYVEPLGAYLHRY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 REFEGDARGVGLVPGAAPSRGGD-----HHPHSMSPAAMLKSRGPVS-GAAMLPHHHH 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 REMEGDSK-----LTAKSSDGSIKKDALGHVGASSSAAEGMGQQGAYNQGMGYMQPQYH 172
                                                                                                                                                  62 QECVSEFISFVTSEASDKCQREKRKTINGDDLLWAMATLGFEDYIDPLKVYLMRYREMEG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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                            10 AGAENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETI
                                                                                                                         70 QECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.8%; Score 391; DB 2; Length 179; 44.6%; Pred. No. 8.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor NF-Y, CCAAT-binding, chain B - maize N; Alternate names: CAAT-box DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Superfamily: transcription factor HAP3
C:Keywords: DNA binding; transcription regulation
F;30-119/Domain: DNA binding #status predicted <DNA>
                                                                                                                                                                                                                                                                                                         122 DIKGSG--KGGESSAKRDGQPSQVSQFSQVPQQGSFS 156
                                                                                                                                                                                                                                               130 DARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-179 <LIX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S22820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 NGDI 176
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A;Gene: At2g37060
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A.Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis that A.Reference number: A71400; MUID:99121113
A.Accession: G71407
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DAA.
                                                                                                                                                                                                                         C;Accession: G71407
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dir P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gis avanaph, T.; Hompel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana N:Alternate names: protein F4P12.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Accession: T45874
R:Bloecker, H: Mewes, H:W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. Sireference number: 223016
A:Reference number: 223016
A:Reference number: 223016
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                                                                                                                                                                  A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFE--- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 CVSEFISFITGEASDKCQREKRKTINGDDLLWAMTTLGFEDYVEPLKYYLQKYREVEGEK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 -----GDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM---LPHHHHHH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TTTAGRQGDKEGGGGGGGGGGGGGGG-------APMYGGGMVTTMGHQFSHH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:Z97336; NID:g2244788; PIDN:CAB10233.1; PID:g2244810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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                                                                      transcription factor, CCAAT-binding, chain A - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: transcription factor HAP3
C;Keywords: DNA binding; transcription regulation
F;20-109/Domain: DNA binding #status predicted <DNA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y match 27.1%; Score 410.5; DB Local Similarity 48.3%; Pred. No. 3e-23; nes 87; Conservative 23. Ministry
                                                                                               N,Alternate names: protein DL3310W
C,Species: Arabidopsis thaliana (mouse-ear cress)
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A;Residues: 1-228 <BLO>
A;Cross-references: EMBL:AL132966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-161 <BEV>
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C; Genetics:
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Best Local Similarity
                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <STO>
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A;Molecule type: DNA
A;Residues: 1-215 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 HHPHSMSP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 GGPKS-SP 158
                                                                                                                                                                                     A; Gene: At2947810
A; Map position: 2
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A;Map position: 2
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A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiLin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein At2938880 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                80 ITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPG 139
                                                                                                                                                                                                                                                        140 AAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHDMQMHAAMYGGTAVPPPAGPP 199
                                                                                                                                                                                                                                                                                                                                                             125 -- SAKGGD------PNAKKDGQSSQNG------QFSQLAHQGPYGNSQVTFPLFSS 166
                                                                                                                  Gaps
                                                                                                                                               20 GANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISF 79
                                                                                                                                                                        68 TIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PAAGAENGSAAGGANNGGAAQQHAAPAIREQDRIMPIANVIRIMRRVLPAHAKISDDAKE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.8%; Score 360.5; DB 2; Length 138; 45.4%; Pred. No. 1.1e-19; ative 29; Mismatches 29; Indels 31
                                                                24.6%; Score 372; DB 2; Length 178; 43.6%; Pred. No. 2.1e-20; Ative 27; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 EGDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 EGDNKGSG------KSGD-----GSNRDAGGGVSGEEM 136
                                                                                                         79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 45.49
Matches 74; Conservative
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-138 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: E84810
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A; Map position: 2
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A;Map position: 2
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                                                              Query Match
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                                                                                     Best Local
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Probable CCAAT-box binding transcription factor (imported) - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84508
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Nature 402, 761-768, 1999 W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter A;Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: G84919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|:|||: :|:|||: ||: |||||| | |||||| | ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
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53.1%; Pred. No. 2.2e-19;
iive 23; Mismatches 26
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Best Local Similarity 53.18
Matches 68; Conservative
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Rivuorio, T.; Maity, S.N.; de Crombrugghe, B.
J. Biol. Chem. 265, 22480-22486, 1990
A;Title: Purification and molecular cloning of the "A" chain of a rat heteromeric CCA A;Reference number: A23692; MUID:91093096
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:M55045; GB:J05701; NID:9203352; PIDN:AAA40887.1; PID:9203353
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C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 26-Aug-1999
C;Accession: JC6080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor NF-Y, CAAT-binding, chain B - chicken
C;Species: Gallus gallus (chicken)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
              transcription factor, CCAAT-binding, chain Al - rat
C,Species: Rattus norvegicus (Norway rat)
C,Date: 04-Oct_1991 #sequence_revision 04-Oct-1991 #text_change 26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: transcription factor HAP3
C;Keywords: alternative splicing; DNA binding; transcription regulation
F;53-142/Domain: DNA binding #status predicted CDNA>
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56.6%; Pred. No. 7.3e-17;
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R;Benoist, C
submitted to the EMBL Data Library, January 1992
A;Reference number: S24469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56.68
Matches 64; Conservative
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A; Residues: 1-180 <BEN>
                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-207 <VUO>
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                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                  C; Accession: A23692
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JC6080
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A23692
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A; Title: Co-evolution from yeast to mouse: cDNA cloning of the two NF-Y (CP-1/CBF) subun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö.
                                                                                                                                      C. Accession: $22817
R.Li, X.Y.; Mantovani, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis, I Nucleic Acids Res. 20, 1087-1091, 1992
A.Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y. A; Reference number: $22816; MUID:92195809
A.Accession: $22817
A.Accession: $28817
A.Accession: $2881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                             N;Alternate names: CAAT-box DNA-binding protein
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C;Reywords: alternative splicing; DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Residues: 1-207 <HOO>
A. Cross-references: GB:X55316; NID:g53362; PIDN:CAA39024.1; PID:g53363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 KTINGEDILFAMSTLGFDSYVEPLKLYLQKFREAMKGEKGIG---GAVTATDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 KTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAAPSRGG 146
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   transcription factor NF-Y, CCAAT-binding, chain B - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.4%; Score 324.5; DB 2
56.6%; Pred. No. 7.2e-17;
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Best Local Similarity
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A;Title: The hapC gene of Aspergillus nidulans is involved in the expression of CCAAT-ccA;Reference number: JC6080; MUID:96285564
A;Accession: JC6080
A;Molecule type: mRNA
A;Residues: 1-186 <PAP>
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NAIternate names: CAAT-box DNA-binding protein
C.Species: Petromyzon marinus (sea lamprey)
C.Species: Petromyzon marinus (sea lamprey)
C.Species: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 26-Aug-1999
C.Accession: S22818 5.78116
Nucleic Acids Res. 20, 1087-1091, 1992
A.Fitle: EVOlutionary variation of the CCAAT-binding transcription factor NF-Y.
A.Reference number: $22816; MUID:92195809
                                                                                                                                                                                                                                                ACCOSS-references: GB:U35341; NID:g1017715; PIDN:AAC49411.1; PID:g1017716 C;Genetics: Accoss - references: GB:U35341; NID:g1017715; PIDN:AAC49411.1; PID:g1017716 C;Genetics: According: Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 TITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGL-VPGAAPSRGGDHHPHSM 153
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submitted to the EMBL Data Library, January 1992
A; Reference number: S78116
A; Accession: S78116
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A; Residues: 1-110,'R',112-209 <BEN>
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A; Residues: 1-209 <LIX>
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B. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, W.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Accession: C86222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE005172; NID: 91922961; PIDN: AAB70405.1; GSPDB: GN00141
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.3%; Score 307; DB 2; Length 139; 55.4%; Pred. No. 8.9e-16; tive 26; Mismatches 15; Indels
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Matches 51; Conserv
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A;Molecule type: DNA
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us-09-435-054-2.rspt

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Search time 22.41 Seconds (without alignments)
1641.267 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                          425026 seqs, 132305027 residues
                                                                                                             October 25, 2001, 09:21:25;
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1514
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_plant:\* sp\_rodent:\*

sp\_organelle:\* sp\_phage:\*

5: 6: 7: 8: 9: 110:

sp\_mammal:\* sp\_mhc:\*

sp\_vertebrate:\*
sp\_virus:\*

sp\_human:\* sp\_invertebrate:\*

sp\_fungi:\*

SPTREMBL\_16:\*
1: sp\_archea:\*
2: sp\_bacteria:\*

Database

LES	Description	09fq10 arabidopsis	081130 arabidopsis	09sfd8 arabidopsis	023634 arabidopsis	Q9fqi3 arabidopsis	023310 arabidopsis			09zqc3 arabidopsis	Q9slq0 arabidopsis		Q9sit9 arabidopsis	O59848 aspergillus	073744 xenopus lae	Q63091 rattus norv	Q00735 emericella	076256 schistosoma	004027 arabidopsis	09vis6 drosophila
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	% Query Match	33.0	32.6	32.6	29.3	29.3	27.1	27.1	24.9	24.6	23.8	23.6	23.4	22.8	21.9	21.4	21.1	20.7	20.3	19.1
	Score	499.5	494	494	443.5	443.5	410.5	410	376.5	372	360.5	357.5	354.5	344.5	331.5	324.5	320	313.5	307	289.5
	Result No.	-	7	e	4	Ŋ	9	7	60	σ	10	11	12	13	14	15	16	17	18	19

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Query Match 33.0%; Score 499.5; DB 10; Length 205; Best Local Similarity 61.3%; Pred. No. 5.3e-33; Matches 103; Conservative 16; Mismatches 24; Indels 25; Gaps

82 GEANERCOREORKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAA 141

142 PSRGGDHHPHSMSPAAMLK-----SRGPVSGAAMLPHHHHHD 179

7

RESULT

133

Dp

δy

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δy

Q9fv58 arabidopsis O17286 caenorhabdi Q9up93 homo sapien O75444 homo sapien Q91ey8 arabidopsis Q9nka2 drosophila Q9v195 drosophila Q9v194 drosophila Q9ual9 drosophila Q92171 gallus gall O13068 xenopus lae O9722 gorilla gor	POYTO UNITED POYOUT BY CONTROL OF 10200 MUST B	ALIGNMENTS  T 1  OPEGJO  PRELIMINARY; PRT; 205 AA.  OPEGJO  O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)  MAGNOI (TREMBLRELL 16, Last update)  MAGNOI (TREMBLELL 16, Last update)  MAGNOI (TREMBLRELL 16, Last update)  MAGNOI (TREMBLRELL 16, Last update)  MAGNOI (TREMBLRELL 16, Last upda	IDE# 3DT303D CNCO#;
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20 260.5 21 260.5 22 1910.5 23 1911 24 190.5 25 185 26 174 29 174 30 160	7 4 4 4 7 T	UT 1  OGPGJO PRELIMINARY; OGFGJO; O1-MAR-2001 (TrEMBLrel. 16, O1-MAR-2001 (TremBlant) ONCBL TANID-3702; ONCBL TANID-3702; CANADARA S., STRAIN-COLUMBIA; Kaneko T., Katoh T., Asamiz, Tababa S., STRAIN-COLUMBIA; SUDMITTER (ARR 1999) to the SMBL, ABOSEO83:1;	SECUEINCE
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Yamaqishi K., Fischer R.L., Goldberg R.B., Harada J.J.;
"Arabidopsis LEAPY COTYLEDONI is sufficient to induce embryo
davelopment in vegetative cells.";
Cell 93:1195-1205(1998).
EMBL, AF036684; AAC39488.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
126F17.20.
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Last annotation update)
                                  208 AA.
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                                                         081130;
01-NOV-1998 (TrEMBLrel, 08, Created)
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Best Local Similarity 47.0%;
Matches 117; Conservative
                                  PRELIMINARY;
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InterPro; IPR000166; -.
InterPro; IPR000947; -.
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Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                                                                                                                                                                                                                                                  Length 208;
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y13724; CAR74052.1; -.
Mendel; 26811. Arath, 2691,26811.
InterPro; IPR000166;
                                                                                                 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                  22679 MW; ODEB469D9F8BEFDC CRC64;
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Last annotation update)
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NCBI_TaxID=3702;
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-OCT-2000 (TrEMBLrel. 15, Last ann
                                                                                                                                                                InterPro; IPR000947; -
Pfam; PF00808; CBFD_NFYB_HMF; 1.
PRINTS; PR00615; CCAATSUBUNTA.
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HSSP; P19267; 1B6W.
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                                                                                                                                                                                                                                                                                 Best Local Similarity
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Best Local Similarity
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                                                     Ecker J.R.;
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SEQUENCE
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                                                                                                                                                     SFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 PGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHHDMQMHAAMYGGTAVPPPAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---RPQTGGEVGEHQRD--AVGDGGGFYGGGGGMQYHQHHQFLHQQNHMYGAT----- 173
                                                                                  65 SFVTGEASDKCQKEKRKTINGDDLLWAMTTLGFEDYVEPLKVYLQRFREIEGERTGLG-- 122
                                                                                                                                 138 PGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHHHHHDMQMHAAMYGGTAVPPPAG 197
                                                                78 SFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLV 137
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18 AGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYI 77
               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                  198 PPHHGGFLMPHPQGSSHYLPYAYEPTYGGEHAMAAYYGGAAYAPGNGGSGDGSGSGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-COLUMBIA;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AR025628; BAB09090.1; - SEQUENCE 190 AA; 20529 MW; DRESCEOF42247C02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.3%; Score 443.5; DB 10; Length 190; 38.7%; Pred. No. 1.6e-28; ive 29; Mismatches 55; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO CCAAT-BOX-BINDING TRANCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                     190 AA
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Matches 94; Conservative
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SEQUENCE FROM N.A. Bloecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Bloecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salancubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 CVSEFISFITGEASDKCQREKRRIINGDDLLWAMTTLGFEDYVEPLKVYLQKYREVEGEK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 TTTAGROCDKEGGGGGGGGGGGGGGGGGG-------APMYGGGMVTTMGHQFSHH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 -----GDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM---LPHHHHHH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 CVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFE--- 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N., Kreis M., Kavanagh T., Entian K.D., Rieger M., James R., Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A., Jones J., Palme K., Ansorge W., Delseny M., Bancroft I., Mewes H.W., Schueller C., Chalwatzis N.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Eukaryothyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicorytedons; core eudicots; Rosidae; eurosids II;
Arassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: 297336; CAB10233.1; -.
EMBL: AL161539; CAB78496.1; -.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSCRIPTION FACTOR NF-Y, CCAAT-BINDING-LIKE PROTEIN
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%; Score 410.5; DB 10;
48.3%; Pred. No. 6.2e-26;
tive 23; Mismatches 35;
                                                                                                                                                        CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A.
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161 AA.
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                                                            Created)
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PRT;
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Pfam; PF00808; CBFD_NFYB_HMF; 1.
PRINTS; PRO00615; CCAATSUBUNTA.
PROSITE; PS006085; CRA_NFYB; 1.
SEQUENCE 161 AA; 17186 MW; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P19267; 1B6W.
Mendel; 26681; Arath;2691;26681.
InterPro; IPR000166; -
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PRELIMINARY;
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                                                                                                                             (TrEMBLrel.
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Best Local Similarity
Matches 87; Conserva
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                                                                01-JAN-1998
                                                                                           01-JAN-1998
01-MAR-2001
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                                 023310;
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                                                                                                                                                                                                                                                                                                           10 AGAENGSAAGGANNGGAAQQHAAPAIREQDRIMPIANVIRIMRRVLPAHAKISDDAKETI 69
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                                                                                                                                                                                                                                            DB 10; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards D., Smith A.G., Murray J.A.;
L Submittee (JUN-1997) to the EMBL/GenBank/DDBJ databases.
R EMBL, Y13723; CAA74051.1; -.
R HSSP, P19267; 1860.
R HSSP, P19267; 1860.
R InterPro: IPR000166; -.
R InterPro: IPR000166; -.
R Ffam, PF00608; CBFD_NFYB_HNF; 1.
R PRINTS; PR00615; CGAATSUBUNTA.
R PROSITE; PS00665; CBFA_NFYB; 1.
SEQUENCE 141 AA; 15181 MM; D33060B5AD21D9E0 CRC64;
                                                                                                                                                                                                                                                                              Indels
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              EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR132966; CAB67641.1; -.
InterPro; IPR000166; -.
InterPro; IPR000161; -.
                                                                                               InterPro; IPR000947; -.
Pfam; PF00808; CBFD_NFYB_HMF; 1.
PR100615; CCAATSUBUNTA.
Probom; PP001367; -; 1.
PROSITE; PS00685; CBFA_NFYB; 1.
SEQUENCE 228 Aa; 25132 MW; BC158AE0A08579B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 EGDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM 170
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                130 DARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 DTKGSG--KGGESSAKRDGQPSQVSQFSQVPQQGSFS 156
                                                                                                                                                                                                                                           Query Match
27.1%; Score 410; DB 1C
Best Local Similarity 49.7%; Pred. No. 1e-25;
Matches 78; Conservative 29; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 141 AA
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SEQUENCE FROM N.A.
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80 ITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPG 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 -- SAKGGD----- PNAKKDGQSSQNG-----QFSQLAHQGPYGNSQVTFPLFSS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                            Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002260; AAD18153.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B3CF497383EC86C4 CRC64;
 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PUTATIVE CCAAT-BINDING TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.6%; Score 372; DB 10; 1
43.6%; Pred. No. 9e-23;
Mismatches 49;
                                                                                         178 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00808; CBFD_NFYB_HMF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRODGIS; CCAATSUBUNTA.
PROSITE; PSODG85; CBFA_NFYB; 1.
SEQUENCE 178 AA; 19523 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                    Mendel; 39697; Arath; 2691; 39697
Conservative
                                                                                       PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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InterPro; IPR000947; -
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Best Local Similarity
Matches 79; Conservat
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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         DEGLINE-20083487; PubMed=10617197;

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Evjii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J. Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Mature 402:701-768(1999).

HSSP; P19267; 186W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TIQECVSEYISFITGEANERCQREQRRTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAAGAENGSAAGGANNGGAAQQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Embryophyta; Tracheophyta, Spermatophyta,
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005309; AAGC3535.1; -.
HSSP; P48781; 1B67.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.8%; Score 360.5; DB 10; Length 138; Best Local Similarity 45.4%; Pred. No. 5.7e-22; Matches 74; Conservative 29; Mismatches 29; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A).
                                                                                                                                                                                                                                    6465C024702AC0F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 EGDNKGSG------KSGD------GSNRDAGGGVSGEEM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 EGDARGVGLVPGAAPSRGGDHHPHSMSPAAMLKSRGPVSGAAM 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).
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InterPro; IPR000947; -.
Pfam; PF00808; CBPD_NFYB_HMF; 1.
PRNTS; PR000615; CCAATSUBUNTA.
PROSTTE; PS00685; CBFA_NFYB; 1.
SEQUENCE 160 AA; 18122 MW; 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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NCBI_TaxID=3702;
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STRAINE-ZO083487; PubMed=10617197;
MEDLINE-ZO083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
R. Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
R. Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
R. Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
R. Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
R. Salzberg S.L., Fraser C.M., Venter J.C.;
R. Sequence and analysis of chromosome II of Arabidopsis thaliana.";
R. Mature 402:761-768(1999).
R. Mature 402:761-768(1999).
R. HSSP; P48718; 1867.
R. InterPro; IPR000165; --
R. InterPro; IPR00047; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 FEGDARGVGLVPGAAPS-----RGGDHHPHSMSPAAMLKSRGPVSGAAMLPHHH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETIQECVSEYISFITGEANERCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYRE 126
                                                                                CQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAAPSRGGD 147
                                                                                                     42 QQEESMMYKEQDRLLPIANVGRIMKNILPANAKVSKEAKETMQECVSEFISFVTGEASDK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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87
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ATZOLISTO.
ATZOLISTO.
ATZOLISTO.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Bagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Arassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 PGVAETNPGSPSSKTNNNNNNN------KEQDRFLPIANVGRIMKKVLPGNGKISKDAK
  QQHAAPAIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00808; CBFD_NFYB_HMF; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PROSITE; PS00685; CPEPTYEY; 1.
SEQUENCE 215 AA; 24619 MW; 0615B2B7A097DD25 CRC64;
                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE CCAAT-BOX BINDING TRANCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                       215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PSPFLPVDHQPF 188
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 23.4%
Best Local Similarity 37.8%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                              148 HHPHSMSP 155
                                                                                                                                                                                                    152 GGPKS-SP 158
                                                                                                                                                                                                                                                                                                                            .9SIT9;
                                                                                                                                                                                                                                                                                                       09SIT9
                                                                                                                                                                                                                                                                   RESULT 12
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  28
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RESULT

Gaps

11;

23.6%; Score 357.5; DB 10; Length 160; 53.1%; Pred. No. 1.2e-21; tive 23; Mismatches 26; Indels 11;

Conservative

Best Local Similarity Matches 68; Conserv

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 GPVGGVSSAPGGRPATAGGFPDAADNTNSIMNPSLDPTEQDP----------- 194
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                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NUCLEAR YCCART-BOX BINDING FACTOR B SUBUNIT NF-YB.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Kato M., Kobayashi T., Tsukagoshi N., Tanaka A., Hashimoto H.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010431; BAA28356.1; -.
InterPro; IPR000166; -.
InterPro; IPR000947; -.
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Herrlor M., Wolffe A.P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF041204; AAC82336.1; -.
HSSP; P48781; 1B67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 RCQREQRKTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFE------
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InterPro; IPR000947; -.
Pfam: PF0008; CBFD_MRYB_HMF; 1.
PRINTS; PR00615; CCAANSUNTA.
PROSITE; PS00685; CBFD_NRYB; 1.
SEQUENCE 206 AA; 22582 MW; 35933B20A6D43607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7A1A74E8F2E05C06 CRC64;
                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%; Score 344.5; DB 3
38.5%; Pred. No. 1.9e-20;
iive 28; Mismatches 48
                              215 AA.
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                                                                                         Created)
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                                                                                01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 38.5%
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The Purification and molecular cloning of the 'A' chain of a rat

The terometric CAAT-binding protein. Sequence identity with the yeast

The HAP3 transcription factor. ".

J. Biol. Chem. 265:22480-22486(1990).

Brinish M6617, AAA4088.1; -.

R HSSP, P48781; 1B67.

R InterPro; IPR000166; -.

R InterPro; IPR000166; -.

Pfam: PF00808; CBFD_MFYB_HMF; 1.

Pfam: PF00808; CBFD_MFYB_HMF; 1.

PROSITE; PR00615; CCAATSUBUNFA.

R PROSITE; PR00615; CAATSUBUNFA.

R PROSITE; PR00615; CBFA_NFYB; 1.
                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                 94 KTITAEDVLWAMSRLGFDDYVEPLGAYLHRYREFEGDARGVGLVPGAAPSRGGD--HHPH 151
                                                              34 AIREQDRLMPIANVIRIMRRVLPAHAKISDDAKETIQECVSEYISFITGEANERCQREQR 93
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   Score 331.5; DB 13; Length 206; Pred. No. 2e-19; 9; Mismatches 42; Indels 3;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COMMENT Contact: Takuji Sasaki	National Institute of A Rice Genome Research Pr 2-1-2 Kannondal, Tsukuba	Ibaraki, Tapan 305	Tel: 0298-38-7441 Fax: 0298-38-7468	Email: tsasaki@abr.affr	PROJECT = 'RGP'. C52742 12A.		source 1695	/strain="culti	/db_xret="taxo /clone="c52742	/clone_lib="Ri	/note="Vector:	oligo(dT) as a	ACT. FINITE			tch 29.48;	Similarity 75.7%;	522;	QY 164 geeggegateegegageaggaeegg		1 6	QY 224 gcgcgtgctgccggcgcacgccaag	Db 61 ccecerecresececeaes	Qy 284 egigicogagiacaicageiteate	Db 121 CGTGTCGGAGTACATCAGCTTCATC	Ov 344 monapagacteropoperation		Db 181 GCGCAAGACCATCACCGCCGAGGAC	Qy 404 ctacgtcgagccgctcggcgcctac	Db 241 CTACGTCGAGCCCCTCGGCGTCTAC	Ov 464 cappatonagettest	DD SOL CASCATCASCATCASCATCASCACC	Oy 524 catgtcgccagcggcgatgctcaag	Db 355 CGGTGGGATGCTCAAG	Qy 584 gcaccaccaccaccacgacatg	Db 397GCACCACGACATG		. !	Db 445 GCGGCGNCGCCGCATCCTCCG	Qy 702 agtagccactacctgccttacgcgt	Db 505 CACGGCCAGTACGCGCCGC	Qy 762 gcatactatggaggcgccgcgtacg	
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r: pBluescript II SK+; Site_1: SalI; Site_2: repared from rice callus mRNAs by using a primer and ligating to the SalI-NotI site at II SK+ phagemid. " 6 others
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HVSMEh0102J16f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0102J16f,
                                                                                                                                                                                                                                                                                                Poaceae; Pooideae
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wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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/ta; Liliopsida; Poales; Poaceae; Pooidea
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Unpublished (2000)
On Aug 21, 2000 this sequence version replaced gi:9860783.
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WCDBANODO9 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 655 7288
Fax: 864 656 4293
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2 q 68
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/db_xref="taxon:4513"
/clone="HVSMEh0102J16f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 512.
Location/Qualifiers
 822 agtggcggcggtggcgggagcgcgtcgcac 851
                                616 GGCAGCGGTGGCGCCGCCGCCGNAGAAC 645
                                                                                                                                                                                                                                                          Hordeum vulgare
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
                                                                                                                                                                                        BE603222 GI:13191083
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                                                                                                                                                                           mRNA sequence.
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Wood,T.
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SOURCE
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                                                                                                     BE603222
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/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
of Spring barley variety 'Barke', a high quality malting
variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
(3'-end of cDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the EcoRI site is NOT present,
as well as the EcoRI adapter. Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 594)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de Seq primer: T3 primer for 5'end.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  AL506199 594 bp mRNA EST 04-JAN-2001
AL506199 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
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397
                                                     354
                                                                                                                                           398 cgacgactacgtcgagccgctcggcgcctacctccaccgctaccgcgagttcgagggcga 457
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338 ggagcagcgaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggctt
                             295 CGAGCAGCCAAGACCATCACCGCGGGGACGTGCTCTGGGCCATGAGCCGCCTTGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A. EST sequencing and analysis in barley Unpublished (2000)
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77.0%; Pred. No. 9.9e-42;
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/db_xref="taxon:4513"
/clone="HY02F18T"
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213 c 1
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/note="Vector: plasmid pBK-CMV; Site_1: ECORI; Site_2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: ECORI (5'-end of CDNA) and XhoI (3'-end of CDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the ECORI site is NOT present, as well as the ECORI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL509098 .441 bp mRNA EST 04-JAN-2001
AL509098 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare cDNA clone HY10L07V 5', mRNA sequence.
AL509098
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                                                                                                                                                                                 396 ttcgacgactacgtcgagccgctcggcgcctacctccaccgctaccgcgagttcgagggc 455
336 cgggagcagcgaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggc 395
                                                                                                                             295 ATGGAGCACCGCAAGACCGTCAACGCGGAAGACATCGTGTGGGCCCTGAACCGCCTCGGC 354
                                                                                                                                                                                                             415 GGGACAGGTGCCGGTGCCGCGACAACGCGCCGCCACAAGGGCGCCCTCCCCGCGCG 474
                                                                                                                                                                                                                                                                                      456 gacgegegegegteggetegteeceggggggeegeeeeategegeggeggegaeeae
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/lab_host="XLOLR"
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Michalek,W.; Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
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/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="txxon:4513"
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156 catgoggcgccggcgatccgcgagcaggaccggctgatgccgatcgcgaacgtgatccgc 215

0; Gaps

19.2%; Score 225.2; DB 105; Length 441; 77.7%; Pred. No. 7.1e-40; tive 0; Mismatches 77; Indels 0;

Matches 269; Conservative

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Similarity

Query Match Best Local 9

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(bases 1 to 497)
Shoemaker, R. Kelin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptco, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3522 FAX:(888) 919-3324 or (314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="differentiating somatic embryos cultered on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG551755 497 bp mRNA EST 09-APR-2001 sad42f11.yl Gm-c1075 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1075-669 5' similar to TR:081130 081130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG. [1] ;, mRNA sequence.
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Rosidae; eurosids I: Fabales; Fabaceae; Papilionoideae; Glycine.
                                                   270 ATGGAGCACCGCAAGACCGTCAACGCGGAAGACATCGTGTGGGCCCTGAACCGACTCGGC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                   90 CAGGCGACGCCGGTGCTGCGGGAGCAGGACCGGCTGATGCCGATCGCGAACGTGATCCGN 149
                                                                                                                                                                                                                                                                                                                                                                                                     396 ttcgacgactacgtcgagccgctcggcgcctacctccaccgctaccgcgagttcgaggc 455
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                     336 cgggagcagcgcaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggc
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Public Soybean EST Project
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synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the ECORI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab, 110 c 131 g 90 t
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146 BASE COUNT

ORIGIN

÷ 244 TICTCCCTCCACACGCAAAAATCTCGGACGATGCAAAGAAACAATCCAAGAGTGCGTGT 303 eggagtacatcagetteateaegggggaggecaaegageggtgeeagegggageagegea 348 169 cgatccgcgagcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcg 228 184 CGGTGAGGGAGCAAGACAGGTTCATGCCAATCGCTAACGTGATTAGGATCATGCGCAAGA 243 349 agaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacg 408 Gaps tgctgccggcgcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgt Score 192.4; DB 155; Length 497; Pred. No. 1.3e-32; 0; Mismatches 61; Indels 0; Query Match 16.4%; Best Local Similarity 79.0%; Matches 229; Conservative ( 229 289 ò В ò g õ g ò

364 AGACCATAACCGCAGAGGACGTGCTTTGGGCCATGAGCTTGGATTCGACGACTACA 423 409 tcgagccgctcggcgcctacctccaccgctaccgcgagttcgagggcgac 458 424 TCGAACCGTTGACCTTCACCGCTACCGTGAACTTGAGGGTGAC 473 g ô g

AW412980 · 551 bp mRNA EST 18-JUL-2000 2030401/10 GENOME SYSTEMS CLONE ID: 8030401/11 VI Gm-c1029-97 5/ similar to TR:081130 081130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG. ; mRNA sequence. AW432980.1 GI:6964287 Glycine max AW432980 soybean. DEFINITION ACCESSION VERSION ORGANISM AW432980 KEYWORDS RESULT rocus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosladae; eurosida I; Fabales; Fabaceae; Papilionoideae; Glycine. (Dases 1 to 551)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,M., Sohurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. AUTHORS REFERENCE

Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project JOURNAL TITLE COMMENT

This clone is available through: Genome Systems, Inc. 4633 World parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Email: est@watson.wustl.edu Fax: 314 286 1810

/ncte="Vector: psport; site\_1: Not I; Site\_2: Sal I; This cond library was constructed from mRNA isolated from very young cotyledons (20-50mgs fresh weight) of greenhouse grown plants. The library was prepared using the Life Technologies psuperscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I sal I restriction site of the pspoRTI vector. The ligated cDNA fragments were transformed into E.coli Electromax DHIOB host cells. This library was constructed by Dr. Paul Keim and Dr. Virinia Coryell." /tissue\_type="very young cotyledons of greenhouse grown www.genomesystems.com 0.00 /clone="GENOME SYSTEMS CLONE ID: Gm-c1029-97" /clone\_lib="Gm-c1029" 104 t info@genomesystems.com web site: Insert Length: 1007 Std Error: /organism="Glycine max" High quality sequence stop: 455 Location/Qualifiers /db\_xref="taxon:3847 144 g /lab\_host="DH10B" 147 c Source BASE COUNT FEATURES ORIGIN

DB 116; Length 551; 16.4%; Score 192.4; DB 1 79.0%; Pred. No. 1.3e-32; Local Similarior nes 229; Conservative Query Match

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0;

61; Indels

0; Mismatches

Matches

169 cgatccgcgagcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcg 228 289 cggagtacatcagcttcatcacggggggggggccaacgagcggtgccagcggggagcagcgca 348 235 ITCTCCCTCCACACGCAAAATCTCGGACGATGCAAAAGAAACAATCCAAGAGTGCGTGT 294 175 CGGTGAGGGAGCAAGACAGGTTCATGCCAATCGCCAACGTGATTAGGATCATGCGCAAGA 234 229 tgctgccggcgcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgt δ ρp

295 CTGAGTACATCAGCTTCATCACAGGTGAGGCGAACGAGCGTTGCCAGAGGGAGCAGCGGGA 354 q

349 agaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacg 408 355 AGACCATAACCGCAGAGGACGTGCTTTGGGCCATGAGCAAGCTTGGATTCGACGACTACA 414 ŏ

409 tegageegeteggegeetacetecacegetacegegagttegagggegae ò qq

DEFINITION ACCESSION AW756413 KEYWORDS VERSION

SOURCE

RESULT

AW756413 591 bp mRNA EST 21-NOV-2000 s121al2.yl Gm-c1036 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1036-1943 5' similar to TR:081130 081130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG.; mRNA sequence. AW756413.1 GI:7685765 AW756413 soybean. EST ORGANISM

Glydine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Glydine.

1 (bases 1 to 591)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thelsing, B., Allen, M., Bowers REFERENCE AUTHORS

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/note="vector: psport; Site_1: NotI; Site_2: SalI; This CDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on mSD 20. The library was prepared using the Life. Technologies psupersoript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restrictions site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the psPDNAT! vector. The ligated cDNA fragments for the psPDNAT! vector. The ligated cDNA fragments site of the psPDNAT! vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Urbana-Champaign. email: l-vodkin@uiuc.edu" nois at l17 c 158 g 113 t
'Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,P., Waterston,R. and Wilson,R.
Public Soybean,EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1036-1943"
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                                                                                                                                                                                                                                                                                                                                                                                                                    info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1034 Std Error: 0.00
High quality sequence stop: 434.
Location/Qualifiers
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Washington University School of Medicine
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BF595304

RESULT

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/ Additions.— United The Page 11 SK+; Site_1: EcoRI; Site_2: AhoI; The CDNA library was constructed from mRNA isolated from mature seed pods of greenhouse grown plants prior to senescence for the cultivar RPI. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended CDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI. XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoRL). This
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bollah, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann. Public Soybean EST Project
Unpublished (1999)
BF595304 470 bp mRNA EST 12-DEC-2000 su76f03.yl Gm-c1055 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1055-653 5' similar to TR:081130 081130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG. [1]; , mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I, Fabales; Fabaceae; Papilionoideae; Glycine.
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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Public Soybean EST Project
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Fax: 314 286 1810
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19 TGAAGGTGTACCTGCAGCGGTTCAGGGAGATGAGGAGAAAAAGGCGTGGCGCGCGTG 20
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Fax: 864 656 4293
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76.6%; Pred. No. 2c...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hordeum vulgare"
/cultivar="C116155 (Mla13)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                         BF263449.2 GI:13260832
                                                            478 tecegggggeegeecat 495
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                                                                                                   19 ATAGGGACGCTCCCTCCT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Yana 153-3. Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Lotus. 1 (bases 1 to 418)
Asamizu,E., Makamura,Y., Sato,S. and Tabata,S. Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 TAAGCTTCATCACCGGGGGAGGCCTCCGACAAGTGCCAGCGGAGAAGCGGAAGACGATCA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 cgcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgtcggagtaca 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 CCGGCGGGGAGCACACGCAGGCGGATCGAACGCTCATGACAGAGATTATCGCTGAAGG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 agcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgcgtgctgccgg 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 cggcgggcggccaacaatggcggcgctgctcagcagcatgcggcgcgcggcgatccgcg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ACGCCGATGACCTGCTGGCCCATGACGACGCTTGGGTTCGAGGACTACGTGGAGCCGC 80
                                                349 agaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggcttcgacgactacg 408
            291 CTGAGTACATCAGCTTCATCACAGGTGAGGCGAACGAGGGTTGCCAGAGGGAGCAGCGGA 350
                                                                                   351 AGACCATAACCGCAGAGGACGTGCTTTGGGCCATGAGCAAGCTTGGATTCGACGACTACA 410
                                                                                                                                                                                                                                                             23-MAY-2000
                                                                                                                                                                                                                                                                   AV424305 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM038e02_r 5', mRNA sequence.
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                                                                                                                             409 togagoogotoggocotacotocacogotacogogagttogagggogacgog 462
                                                                                                                                                  411 TCGAACCGTTGACCATGACCTTCACCGCTACCGTGAACTTGAGGTGACCGCAC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM038e02_r"
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                                                                                                                                                                                                                                                                                                                                              AV424305.1 GI:7781090
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 595)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Wing,R., Close,T.J., Henry,D., Kernodle,S., Palmer,M., Rambo
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
       BF263449 595 bp mRNA EST 09-MAR-2001
W. CEROMORNIOH HOArdeum vulgare seedling green leaf EST library
HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CBA0006M10f, mRNA sequence.
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199 c 173 g 87 t 3 others
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09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db.cref="taxon:4513"
/db.cref="taxon:4513"
/clone="HV_CEa0006M10f"
/clone_lib="Hordeum vulgare seedling green leaf ES
library HVCDNA0004 (Erysiphe infected & control)"
/library HVCDNA0004 (Erysiphe infected & control)"
/library HVCDNA00121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for barley genomics Unpublished (2000) On Novi 17, 2000 this sequence version replaced gl:11194443 Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 187; DB 146; Length 595;
Pred. No. 2e-31;
0; Mismatches 70; Indels 0;
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Query Match
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'Triticaee, Hordeum.
'Dases I to 595)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
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                                                                                                                                                               BF263455 . 595 bp mRNA EST 09-MAR-2001
HV CEa0006M16f Hordeum vulgare seedling green leaf EST llbrary
HVCDNA00004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV CEa0006M16f, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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295 GAGAAGCGCAAGACCATCAACGGCGACGACCTGCTCTGGGCAATGACCACCCTCGGCTTC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="C116155 (M1a13)"
/cultivar="C116155 (M1a13)"
/clone_lib="HyCEaO006M16f"
/clone_lib="Hordeum vulgare seedling green leaf EST
/tissue_type="Seedling green leaf"
/tissue_type="Seedling green leaf"
/lab_host="TJC121"
                                  for barley genomics
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11194449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 595; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 187; DB 146;
Pred. No. 2e-31;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seg primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 590.
Location/Qualifiers
                                                                                                                                                                                                                                                           BF263455.2 GI:13260837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.98;
76.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
                                                                                                                                                                                                                                                                                                                   Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity,
                                                                                                                                                                                                                                                                                                  barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                            RESULT 11
                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                  BF263455
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                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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Bukaryoum aceltvum

Bukaryothyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wignollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

Thases I to 924)

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Engridge, P., Lazo, G.K., Lin, J.J., McGuire, P., Ogihara, Y., Sorchlis, M., Warburton, M. and Wenzel, G., Shariflou, M., Schuch, M., Selvaraj, G., Shariflou, M., Marburton, M. and Wenzel, G.

Expressed Squence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Lissue_Lype="young leaf"
/dev_stage="after 24 hour challenge with LR-AVR1"
/note="vector: Lambda ZAP; 1.0 Kbp average insert size."
233 c 240 g 189 t 48 others
                                                                                                                                                                                                           BE418716 924 bp mRNA EST 24-JUL-2000 SCL074.B01R990724 ITEC SCL Wheat Leaf Library Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 caggagtgcgtgtcggagtacatcagcttcatcacgggggaggccaacgagcggtgccag 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 cgggagcagcgcaagaccatcaccgccgaggacgtgctgtgggccatgagccgcctcggc 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 catgoggoggoggogatcogcgagoaggacoggotgatgcogatcgcgaacgtgatccgc 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 atcatgcggcgcgtgctgccggcgcacgccaagatctcggacgacgccaaggagacgatc 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 CAGGAGTGCGTCTCCGAGTTCATCTTCTTCATCACCGGCGAGGCCTCCGACAAGTGCCAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 gccggcgcggagaatggctcggcggcggcggcgacaatggcggcgctgctcagcag 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 ATCATGAAGAAGGCGCTCCCGGCCAACGCCAAGATCAGCAAGGACGCCAAGGAGACGGTG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 CTGTCATCGCCG-----CGGGAGCAGGACCGCTTCCTGCCCATCGCCAATGTCAGCCGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cereal Research Centre, Agriculture & Agri-Foods Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="ITEC SCL Wheat Leaf Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%; Score 185.2; DB 1
illarity 70.1%; Pred. No. 5.1e-31;
Conservative 0; Mismatches 106

    .924
    /organism="Triticum aestivum"

                                                                                                                                                                                                                                                                         cDNA clone SCL074.B01, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://wheat.pw.usda.gov/genome_
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="SCL074.B01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                        BE418716.1 GI:9416562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Winnipeg MT CANADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cloutier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 983 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
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/dote="Vector: pBluescript II SR+; Site_I: ECORI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels with distilled
water. The cotyledons were flash-frozen in liquid
nitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthesize the cDNA. First- stranded synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor
nucleotide (V-A, C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGACTAGTCTCGAG(T)] is anchor
the county of the contract of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sf09g11.V1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-1821 5' similar to TR:023310 023310 CCAAT-BINDING AW201996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enkaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosladae; eurosida; Fabales; Fabaceae; Papilionoideae; Glycine. 1 (bases 1 to 500)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bollab, Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                            396 ttcgacgactacgtcgagccgctcggcgcctacctccaccgctaccgcgagttcgagggc 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the primer at the 5' end of the poly(A) tract. After second- strand synthesis, the cDNA ends were filled in
265 CGCGAGAAGCGCAAGACCATNAACGGCGACGAGCTGCTCTGGGCCATGACCACCTCGGC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="cotyledons of 3- and 7-day-old Williams seedlings"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                             /organism="Glycine max"
/db_xref="taxon:3847"
/dlone="GENOME SYSTEMS CLONE ID: Gm-c1027-1821"
/clone_lib="Gm-c1027"
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Insert Length: 1004 Std Error: 0.00
High quality sequence stop: 411..
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:6482782
                                                                                                                                                                                                                                                                                      456 gacgcgcgcgcgtc 470
                                                                                                                                                                                                                                                                                                                                                                              385 NAGAGGCCGCCGCC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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AW201996.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max
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JOURNAL
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SOURCE

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subsequently phosphorylated. The XhoI suber within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500 bp cutoff, using Gibrobalt Life Technologies' CDNA Size Fractionation column. The column cluent was then ligated into Stratagene's paluescript(tm) II XR Predigested vector (pRluescript II SK(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene); 97% of the plasmids with CDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia CDTypell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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Shoemaker, W., Keim.P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
Y., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
Y., Waterston, T., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF715909 431 bp mRNA EST 02-JAN-2001 saalle08.yl Gm-c1058 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1058-999 5' similar to TR:023310 023310 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 gegeeggegateegegageaggaeeggetgatgeegategegaaegtgateegeateatg 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 GAGATGTCGCCGCGGGAGCAGGACCGGTTCCTGCCGATCGCGAACGTGAGCCGCATCATG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 AAGAAGGCGCTGCCGGCGAACGCGAAGATCTCGAAGGACGCGAAGGAGGAGGTGCAGGAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 tgcgtgtcggagtacatcagctt--catcacggggaggccaacgagcggtgccagcggg 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 TGCGTGTCGGAGTTCATCAGCTTTCATTCACCCGCGAGGCCTCCGACAAGTCCCAGCGGG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 agcagcgcaagaccatcaccgccgaggacgtgctgtggggccatgagccgcctcggcttcg 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AGAAGCGCAAGACGATCAACGGCGACGACCTGCTGGGCGATGACCACTCTCGGCTTCG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 acgactacgtcgagccgctcggcgcctacctccaccgctaccgcgagttcgagggcga 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine.
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
with cloned Pfu DNA, ligated to EcoRI adapters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 cggcgcgctgccggcgcacgccaagatctcggacgacgaggagagaccaaggagagccaaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 113; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 184.8; DB 1
Pred. No. 6.1e-31;
0; Mismatches 62
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78.5%;
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BF715909
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KEYWORDS
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                          SOURCE
                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: Xhoi; The cDNA library was constructed from mRNA isolated from hypocotyl tissue of 2 week old etiolated seedlings for P1468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a ANNI restriction site. EcoRI adapters were ligated to the CDNA fragments followed by Xhoi digestion. The CDNA fragments directionally cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EcoRI-XhoI restriction site of the pBluescript vector. The ligated CoDNA fragments were transformed into DH10B host cells (Gibboo BEL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $158b03.yl Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-5478 5' similar to TR:023310 023310 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A. ;, mRNA sequence.
                                           Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                       /tissue_type="Hypocotyl, 2 week old seedlings, etiolated"
/lab_host="DH10B"
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AAGGGCAAGACCATCAACGGCGACGATCTTCTGGGCCATGACAACCCTGGGATTCGAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgcgtgtcggagtacatcagcttcatcacggggggaggccaacgagcggtgccagcgggag 341
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                                                                                                                                                                                                       /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1058-999"
/clone_lib="Gm-c1058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 180; DB 168; Length 431;
Pred. No. 7e-30;
0; Mismatches 125; Indels 0;
                                                                                                               info@genomesystems.com web site: www.genomesystems.com
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                                                                                                                                     High quality sequence stop: 354.
Location/Qualifiers
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AW760103.1 GI:7691987
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Best Local Similarity 67.1%;
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ORIGIN
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/note="Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
XhoI: This CDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels with distilled
mitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for CDNA synthesis. Stratagene's CDNA
Synthexix Kit (catalog number 200401) was used to
synthesize the CDNA. First- stranded synthesis was
performed with 5-methyl GTTP, hence the ligated CDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor
nucleotide (V-A, C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAACTAGTCTCGAG(T)18] to anchor
the primer at the 5' end of the poly(A) tract. After
second- strand synthesis, the CDNA ends were filled in
with cloned Pfu DNA, ligated to EcoRi adapters and
subsequently phosphorylated. The KhoI site within the
first-strand synthesis primer was then restricted by
digestion with Aho! all XhoI sites in the CDNA would be
protected by their hemimethylated status. The CDNA
constructs were size-fractionated with a 500 bp cutoff,
using GibcoBR. Life Technologies' CDNA Size Fractionation
column - The column eluent was then ligated inco
                                                                                                                                                                                             (bases 1 to 422)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watcon.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-5478"
/clone_lib="Gm-c1027"
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Insert Length: 841 Std Error: 0.00
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Public Soybean EST Project
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Glycine max
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                                                      Gaps
    DB 120; Length 422;
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Query Match 15:3%; Score 179.6; DB 120; Lengt Best Local Similarity 66.8%; Pred. No. 8.6e-30; Matches 254; Conservative 0; Mismatches 126; Indels
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161	83
102 geggagaatggeteggeggeggeggegeeceaeaatggeggegetegeteageageatgeg 161	30 GCTGAGTCGGACAACGACTCGGGAGGGGCGCAGAACGCGGGAAACAGTGGAAACTTGAGC 89
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Search completed: October 25, 2001, 11:39:18 Job time: 3538 sec

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nilarity: 80.335
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                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                             seq_name: gb_est30:AU088581
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US-09-435-054-2 x AU088581
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                                        gb_est54:AW980494
gb_est51:AW738727
gb_est51:AW760103
gb_est49:AW621652
               est26:AI900024
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BE59725.2 su96c06.y1 Gm-c1056 G1
BE516510 WHE611_D10_H192A Wheat
AW77563 EST33468B DSIL Medicaq
BE415647 SCU001.E10.R990714 ITE
AW733618 SK75h06.y1 Gm-c1016 G1
BE600015 sn39h06.y1 Gm-c1004 G1
                                                                                                                                                                                                Command line parameters:
-MODEL-frame+_p2n.model -DEV=xlh
-Q-GG02_LVGFPQ_SEPO1/NO990435054/runat_25102001_085522_6964/app_query.fasta_1.338
-Q-GG02_LVGFPQ_SEPO1/NO990435054/runat_25102001_085522_6964/app_query.fasta_1.338
-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -GAPOP-12.000 -GAPEXT=4.000
-GAPEXT=0.100 -LOOPEL-0.000 -LOOPEXT=0.500 -FGAPOP=6.000
-GARPEXT=7.000 -YGAPOP-10.000 -XGAPEXT=0.500 -DELOP=6.000
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                                                                                                                        Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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.2e-20
.2e-20
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Database length: 431459454
Search time (sec): 1006.350000
                                                              Date: Oct 25, 2001 2:03 PM
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Query length: 278
Database: EST:*
                                                                                                                  About: Results were
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9b_est176:8E603222

9b_est10:8G551755

9b_est10:8G551755

9b_est20:8F595304

9b_est21:8A1506199

9b_est21:8A1506199

9b_est21:8A150908

9b_est21:8A150908

9b_est21:8A18716

9b_est21:8A18716

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9b_est85:8F534455

9b_est85:8F534455

9b_est85:8F534455

9b_est19:8E803572

9b_est19:8E803572

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gb_est100:BG445358
em_estpl5:AW730639
gb_est99:BG314203
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9b_est99:BG362333
9b_est46:AW35227
gb_est91:BF715909
9b_est50:AW719547
gb_est50:AW720671
gb_est49:AW597630
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gb_est71:BE210041
gb_est90:BF597252
gb_est75:BE516510
gb_est74:BE413647
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gb_est21:AI495007
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A1900024 sb97g11.y1 Gm-c1012
AW980494 EST391647 GVN Medic
AW738727 EST340154 tomato f1
AW760103 s158b03.y1 Gm-c1027
AW621652 EST312450 tomato ro
                                                                                                                                                 seq_documentation_block:
LOCUS AU088E81 695 bp mRNA EST 31-MAR-2000
DEFINITION AU088S81 Rice callus Oryza sativa subsp. japonica cDNA clone C52742
                                                                                                                                                                                                                                                                                                          Oryza sativa subsp. japonica
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa subsp. japonica"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 gIleMetArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ysGluThrIleGlnGluCysValSerGluTyrIleSerPheIleThrGly 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 GluAlaAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGl 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CCGCCTATACGTGAGCAGGACCGGCTGATGCCGATCGCGAACGTGATCCG
                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 695)
Sasaki,T. and Yamamoto,K.
Rice CDNA from callus (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 ProAlaIleArgGluGlnAspArgLeuMetProIleAlaAsnValIleAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 239
Gaps: 10
Percent Identity: 70.293
  4.4e-20
4.8e-20
4.6e-20
3.2e-20
4.6e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tsasaki@abr.affrc.go.jp
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                          Oryza sativa subsp. japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
524.26
523.54
523.91
526.78
523.89
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Ibaraki,
                                                                                                                                                                                                                                                 AU088581.1 GI:7378310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
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177 sHisAspMetGlnMetHisAla 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                           97
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                                                                                                                                                                            source
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                                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for barley genomics
Unpublished (2000)
On Aug 21, 2000 this sequence version replaced g1:9860783.
Contact: Wing RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 sProHisSerMetSerProAlaAlaMetLeuLysSerArgGlyProValS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 GlySerGlyAspGlySerGlySerGlyGlyGlyGlyGlyGly.....se 258
                                                                 99 uAspValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValGluP 116
                                                                                                                                                   116 roLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArg 132
                                                                                                                                                                                                                                          133 GlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHi 149
                                                                                                                                                                                                                                                                                                                                                                                                                  166 erGlyAlaAlaMetLeuProHisHisHisHisHisAspMetGlnMet 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 CCATGGTGACG......CACCACGACATGCAGATG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 o.. HisHisGlyGlyPhe.....LeuMetProHisProGlnGlySerSe 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 rHisTyrLeuProTyrAla .....TyrGluProThrTyrGlyGlyGluH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 GCACCACGCCAGTACGCGCCGCGTACGAC...ATGTACGGCGGCGAGC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 isalametalaalaTyrTyrGlyGlyAlaAlaTyrAlaProGlyAsnGly 244
152 GAGGCCAACGAGCGTGCCAGCGCAACGAAGACCATCACCGCCGA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 GCCNACGGGAGCGGCAGCAGCGGCAGCGTGGCGCCGGCACGCCGNAGAA 644
                                                                                                                                                                            252 CCTCGGCGTCTACCTCCACCGCTACCGCGAGTTCGAGGGGGGAGTCCCGC
                                                                                      202 GGACGTCTGGGCCATGAGCCGCTTCGGCTTCGACGACGACGTCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 TGGTCAC.....GTCGGTGGGATGCTCAAGTCCCGCGCGCAGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est76:BE603222
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BE603222
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181 c 182 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrArgGluPh 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 ysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeuGlyPhe 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 GACGACTACGTCGAGCCCCTCAGCATCTACCTCCACCGCTTCCGCGAGTT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 rgGlyGlyAspHisHisProHisSerMetSerProAlaAlaMetLeuLys 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 SerArgGlyProValSerGlyAlaAlaMetLeuProHisHisHisHisHi 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 lealaasnValIleargIleMetArgArgValLeuProAlaHisAlaLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IleSerAspAspAlaLysGluThrIleGlnGluCysValSerGluTyrIl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuMetProI
                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 174
Gaps: 5
Percent Identity: 71.264
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                             1. .528
∕organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 528
                                                                    Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 512.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            598.50
4.215
81.609
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US-09-435-054-2 x BE603222
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US-09-435-054-2 x AW756413
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                                                                                                                                                                             AW756413 591 bp mRNA EST 21-NOV-2000 s121a12.y1 Gm-c1036 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1036-1943 5' similar to TR:081130 081130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stephce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 Faxx:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
Info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1034 Std Error: 0.00
High quality sequence stop: 434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="somatic embryos cultured on MSD 20"/lab_host="DH10B"
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   505 CGCCGACATGCAGATGCACGCC 526
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                                                                               seq_name: gb_est51:AW756413
                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max
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Percent Identity: 57.062 Length:

3.644

Percent Similarity:

Quality: 481.00

alignment\_scores:

Ratio:

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine. I (bases: Lto 497)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Sohurk, R., Ritter, E., Kohn, S., Shir, T., Jackson, Y., Cardenas, M., McCann, Publis, Sypban, Est Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 .....TGCACGTGAGGGAGCAAGACAGGTTCATGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 PheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrArgGl 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 aAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAsPArgLeuMetP 43
                                                                                                                                                     43 rolleAlaAsnValIleArgIleMetArgArgValLeuProAlaHisAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 uPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAlaAlaProS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 erargGlyGlyAspHisHisProHisSerMetSerProAlaAlaMetLeu 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 LysSerArgGlyProValSerGlyAlaAlaMetLeuProHisHisHisHi 176
                                                                                                                                                                                                                                                                                                                                                           76 rileserPheileThrGlyGluAlaAsnGluArgCysGlnArgGluGlnA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517 ......GGTGTTGCTACTGCTATTGTGCCTCCACCTATCA 551
                                                                                                                                                                                                                                                           60 LyslleSerAspAspAlaLysGluThrIleGlnGluCysValSerGluTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 TCACCACATGGGTAACTTGGTGCTGCCATG 582
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LOCUS BG551755
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361 GGAAGACCATAACCGCAGAGGACGTGCTTTGGGCCATGAGCAAGCTTGGA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab, Iniversity of Illinois)."
                                                                                                                                                                                        This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="differentiating somatic embryos cultered on
     Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="GENOME SYSTEMS CLONE ID: Gm-c1075-669"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LysileSerAspAspAlaLysGluThrileGlnGluCysValSerGluTy 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 rlleSerPhelleThrGlyGluAlaAsnGluArgCysGlnArgGluGlnA 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 rolleAlaAsnValIleArgIleMetArgArgValLeuProAlaHisAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAl 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 74.380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: BG551755 from: 1 to: 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Illinois).
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3847
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
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87.603
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                   COMMENT
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/ncce="Vector: pSDORT1; Site_1: Not I; Site_2: Sal I; This cDNA library was constructed from mRNA isolated from very young cetyledons (20-50mgs fresh weight) of greenhouse grown plants. The library was prepared using the life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli Electromax DHIOB host cells. This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell.
                                                                                                                                                                                                                                                                                                                                                            S103a01.y1 Gm-c1029 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Cm-c1029-97 5' similar to TR:081130 081130 CCAAT-BOX BINDING FACTOR HAD3 HOMOLOG. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker, R. Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Glyclne.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1029-97"
/clone_lib="Gm-c1029"
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Insert Length: 1007 Std Error: 0.00
Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW432980
AW432980.1 GI:6964287
                                                                                                                                                                                                                                                                           seq_name: gb_est47:AW432980
                                                                                                                                         126 uPheGluGlyAsp 130
                                                                                                                                                                                                            461 ACTTGAGGGTGAC 473
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                             129 GCATCATCAGATCACAGCCACAGGAGAGGAGAACGAA.....170
                                                                                                                                                                                                                                                                                                                                           171 .....TGCACGGTGAGGAGCAAGGTCATGC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                  rgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeuGly 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AAAATCTCGGACGATGCAAAAGAAACAATCCAAGAGTGCGTGTCTGAGTA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrArgGl 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LysIleSerAspAspAlaLysGluThrIleGlnGluCysValSerGluTy 76
                                                                                                                                                                                                                     10 AlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAl 26
                                                                                                                                                                                                                                                                                                                                                                                                 43 rollealaasnVallleArgileWetargArgValLeuProAlaHisAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 rIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgGluGlnA 93
                                                                 Percent Identity: 74.380
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                       465.50
4.392
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LOCUS BF595304
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// Anote="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from mature seed pods of greenhouse grown plants prior to senescence for the cultivar KPl. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI.XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                 Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 420.
                                                                                                                                                                                                                                                                                                                                      /tissue_type="Mature seed pods, greenhouse grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                  /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1055-653"
/clone_llb="Gm-c1055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 .....TGCACGGTGAGGAGCAAGGTCATGC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 rgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeuGly 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 rollealaasnVallleargileMetargArgValLeuProAlaHisAla 59
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Fax: 314 286 1810
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US-09-435-054-2 x BF595304
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seg_documentation_block:
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AUTHORS
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/note="Vectors lasmid pBK-CMV: Site_1: ECORI; Site_2: XhOI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of CDNA) and XhOI (3'-end of CDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5' and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp" 85 t 2 others
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                  Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Dipublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Email: michalekelpk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare"
/cultivar="Barke"
/db_xef="taxon:4513"
/clone="HYOF18T"
/clone="HYOF18T"
/clone="HYOF18T"
/tlssue_type="developing caryopsis (3.-15.DAP)"
/tlssue_type="developing caryopsis (3.-15.DAP)"
                                                                                          seq_documentation_block:
LOCUS ALS06199 594 bp mRNA EST 04-JAN-2001
DEFINITION ALS06199 Hordeum vulgare Barke developing caryopsis (3.-18.DAP)
Hordeum vulgare CDNA clone HY02F18T 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGl 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 53.368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AL506199 from: 1 to: 594
                                                                                                                                                                                           AL506199
AL506199.1 GI:12032414
                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 594)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 446.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 594
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US-09-435-054-2 x AL506199
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                                                                                                                                                                                                                                                                                        Hordeum vulgare
                                          seq_name: gb_est28:AL506199
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448 ACTIGAG 454
                                                                                                                                                                                                                                                                    barley.
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JOURNAL
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                                                                                                                                                                                                                                                                    SOURCE
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/organism="Pinus taeda"
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/clone="PC04B12"
/clone="pc04B12"
/clone="Pc04B12"
/clone="Pc04B12"
/clone="Pc04B12"
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/clone="Pc04B12"
/clone="Pc04B12"
/clone="Organ: pollen cone; Vector: Lambda TriplEx; Site_1: Anote="Organ: pollen cones were collected in the early spring, frozen and used for mRNA isolation. The SNART-PCR method (Clontech) was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. I (bases I to 535)
Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R. The Pine Gene Discovery Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW754604 535 bp mRNA EST 01-MAY-2000 PC04B12 Pine TriplEx pollen cone library Pinus taeda cDNA clone PC04B12, mRNA sequence.
AW754604 AW754604.1 GI:7676324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 GTTGCAGGTACTGCAAGCGTCCATGTACGCGCCCCGTCTCCGGTGCAGC 550
                                                                                                                                                                                                                                                                              302 ACCGCAAGACCGTCAACGCGGAAGACATCGTGTGGGGCCCTGAACCGCCTC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 roSerArgGlyGlyAspHisHisProHisSerMetSerPro...... 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 CCACGAGGGCGCCTCCCCGCGCGCGCC.GNCCGCTCTCCACGCCGTGCC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ........ AlaAlaMetLeuLysSerArgGlyProValSerGlyAlaAl 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 aMetLeuProHisHisHisHisHisAspMetGlnMetHisAlaAlaM 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 T.....CAGAATCACATTGCNA 567
252 GITCATCAGCITCGTCACCGGCGAGGCCAACGAGGGGGGGGGTGCCACATGGAGC 301
                                                                                                                                                                                                                                       92 lnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeu 108
                                                                                                                                                                                                                                                                                                                                                                             109 GlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrAr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                         352 GGCTTCGACGACTACGTCCTGCCCTCAGCGTCTTCCTGCACCGCATGCG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 gGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAlaAlaP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 CGAGGGCGAGGGGGGACAGGTGGTGCCGGTGCAGGCGACAACCGCGCCG 451
                                                                                                     75 uTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgGluG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 GA.....GGCCAGTTGTACGCGCCCCC 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 etTyrGlyGlyThrAlaValProProPro 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est51:AW754604
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prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox exclision in E. coli strain BM25.8 and sequenced from the 5' end."
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Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Ross Whetten
Forest Blotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AM981720 526 bp mRNA EST 02-JUN-2000 PCL5H07 Pine TriplEx pollen cone library Pinus taeda cDNA clone PCL5H07, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 AlaAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAs 100
                                                                                                                                                                                                                                                                                                                                34 AlalleArgGluGlnAspArgLeuMetProlleAlaAsnVallleArgIl 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 luThrIleGlnGluCysValSerGluTyrIleSerPheIleThrGlyGlu 83
                                                                     21 others
                                                                                                                                                                                                                                                                                                                                                                                   eMetArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NC. 27695-8000
Tel: 919-515-7800
Fax: 919-515-7801
Email: rosswhete/unity.ncsu.edu
Seq primer: 5' lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 euGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArg 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 82.828
                                                                    139 t
                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                              Align seg 1/1 to: AW754604 from: 1 to: 535
                                                                129 g
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                                                                  103 c
                                                                                                                                                                     4.585
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US-09-435-054-2 x AW754604
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LOCUS AW981720
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                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                    alignment_scores:
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DEFINITION
                                                                BASE COUNT
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COMMENT
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KEYWORDS
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//lab_host="E. coli BM25.8"
//lab_host="E. coli BM25.8"
//lab_host="E. coli BM25.8"
//lab_host="E. stil (B); Immature pollen cones were
sollected in the early spring, frozen and used for mRNA
isolation. The SMART-PCR method (Clontech) was used to
prepare a library from 1 ug total RNA, using the Lambda
TriplEx vector. Plasmid subclones in prriplEx were
recovered by cre-lox excision in E. coli strain BM25.8 and
sequenced from the 5' end."
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Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases I to 441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL509098 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY10L07v 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04 - JAN - 2001
/clone_lib="Pine TriplEx pollen cone library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 lnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrAr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 GGTTTTGACAATTACATGGATCCATTGACTCTTACCTTCAGAGATATAG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 GCTTCAATGGCAGAAGATGCAAGCCCAACCAGCCAGGATAACAGCACCTC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 yAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 etProllealaAsnVallleArgIleMetArgArgValLeuProAlaHis 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 uTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgGluG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGl 25
                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 68.595
                                                                                                                                                                                                                                                                                                                                                                  Length:
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                                                                                                                                                                                                                                                                                                                                                                                3.944
88.430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AW981720
                                                                                                                                                                                                                                                                                                                                                           422.00
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US-09-435-054-2 x AW981720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 AGGTATTGAGGGT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
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                                                                                                                                                                                                                                               176
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KEYWORDŞ
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/clous_dilverv,
/clous_inb=Thordeum vulgare Barke developing caryopsis
(3.-15.DAP)"
/tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
/note="Vector: plasmid pBK-CMV; Site_1: ECORI; Site_2:
/note="Vector: plasmid pBK-CMV; Site_1: ECORI; Site_2: DAP)
of spring barley variety 'Barke', a high quality malting
variety. Cloning sites: ECORI (5'-end of cDNA) and XhoI
/3'-end of cDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the ECORI site is NOT present,
as well as the ECORI adapter. Average insert size is lkb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp;
                                                                                Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: mitchalekelipk gatersleben.de, http://pgrc.ipk-gatersleben.de Seg primer: T3 primer for 5'end. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAlaAlaP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTyrAr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 lnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArgLeu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 ACCGCAAGACCGTCAACGCGGAAGACATCGTGGGCCCTGAACCGACTC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 GGCTTCGACGACTACGTCCTGCCCTCANCGTCTTCCTGCACCGNATGCG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 yAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AlaLysIleSerAspAspAlaLysGluThrIleGlnGluCysValSerGl 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 uTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgGluG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GCCCTAGCCATGGAGAACTTCAACGTCCCGAACGGAGCA.....GCGGC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 2
Percent Identity: 57.823
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
/cultivar="Barke"
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                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 g
                                                                                                                                                                                                                                                                                                                                                /clone="HY10L07v'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417.50
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US-09-435-054-2 x AL509098
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  TITLE
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Friticum destruum
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
; Triticeae; Triticum.
; Triticeae; Triticum.
; Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feulllet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jab,J., Jouditer,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Sharifilou,M., Sorrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS BE418716 924 bp mRNA EST 24-JUL-2000
DEFINITION SCL074.B01R990724 ITEC SCL Wheat Leaf Library Triticum aestivum CDNA clone SCL074.B01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cereal Research Centre, Agriculture & Agri-Foods Canada
Winnipeg MT CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 nHisAlaAlaProAlaIleArgGluGlnAspArgLeuMetProIleAlaA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGlnGl 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 snVallleArgIleMetArgArgValLeuProAlaHisAlaLysIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 6
Percent Identity: 38.710
142 roSerArgGlyGlyAspHisHisProHisSerMetSerPro 155
                                          ......GCAGGCGACAACCGCGCCGCCACGAGGGCGCCT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
/cultivar="Thatcher Lr1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                   BE418716.1 GI:9416562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cloutier S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 204 983 2340
Fax: 204 983 4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410.00
2.715
60.887
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                                                                                            seq_name: gb_est74:BE418716
                                                                                                                                                                                                                                                                                                     bread wheat.
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                                               408
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4633 World Parkway Circle, St. Louis, MO 63134, USA et 1877-577-2733 Fax: 314 427-324 Email: service@genomesystems.com.
                                                                                                                                                                       /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="701502287"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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                                                                                                                           Location/Qualifiers
1. .575
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         Pharmaceuticals, Inc
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US-09-435-054-2 x AI995140
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Ratio:
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Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 leThrAlaGluAspValLeuTrpAlaMetSerArgLeuGlyPheAspAsp 112
                                                                                                                                                                                                                    113 TyrvalGluProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGl 129
                                                                                                                                                                                                                                                                                                                                                                                  129 yAspAlaArgGlyValGlyLeuValProGlyAlaAlaProSerArgGlyG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 lyAspHisHisProHisSerMetSerProAlaAlaMetLeuLysSerArg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....ATGCCAAGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GlyProValSerGlyAlaAlaMetLeuProHisHisHisHisHisAs 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 AACAACAACAACAATGCCCGCCGGTTACCCCGACGCCCCGGGAGGCATGA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pMetGlnMetHisAlaAlaMetTyrGlyGlyThrAlaValProProA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 laGlyProProHisHisGlyGlyPheLeuMetProHisProGlnGlySer 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 SerHisTyrLeuProTyrAlaTyrGluProThrTyrGlyGlyGluHisAl 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 aMetAlaAlaTyrTyrGlyGlyAlaAlaTyrAlaProGlyAsnGlyGlyS 246
                                              184 AAGGACGCCAAGGAGGACGCTGCAGGAGTGCGTCTCCGAGTTCATCTCCTT 233
63 AspAspAlaLysGluThrIleGlnGluCysValSerGluTyrIleSerph 79
                                                                                                                                                                                                                                                                                                                              334 TATGTCGACCCGCTCAAGCACTACCTNCACAAGTTCCGCGAGATCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 ......AACATNAAAATTGCAATGGGGAGGGAAAG
                                                                                             elleThrGlyGluAlaAsnGluArgCysGlnArgGluGlnArgLysThrI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......GATGATGGGGCAGCCCATGTACCGG
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116 c 177 g 118 t 10 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 AAAGTTTACTTGCAGAGGTTTAGGGAGATCGAAGGGGAGAGACTGGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 lGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHisProH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 isSerMetSerProAlaAlaMetLeuLysSerArgGlyProValSerGly 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AlaAlaMet...LeuProHisHisHisHisHisHisAspMetGlnMetHi 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 NNGTGTNGTGGGATGCAGTATCACCAACATCATCAGTTTCTTCACCAGCA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 sAlaAlaMetTyrGlyGlyThrAla.....v 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::: ||||||| :::||||::: 486 GACCCATATGTATGAGCCACACANGTNGAGC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 aAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAspV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgGlyVa 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AGGGAG......GCACAGACTGGTGGTGAGGTCGGAGAGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 ATCAGAGAGGTGCTGTCGGA.....GATGGCGGGTGGGTCTACGGT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 etArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGlnGlnHisAlaAlaProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 alleArgGluGlnAspArgLeuMetProlleAlaAsnVallleArgIleM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 ThrIleGlnGluCysValSerGluTyrIleSerPheIleThrGlyGluAl
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                                                                                                                               HV_CEB0006M10f Hordeum vulgare seedling green leaf EST library
HVCDMA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEB0006M10f, mRNA sequence.
BF263449.2 GI:13260832
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
1. Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 595)
Mugy R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Chol, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wood,r. Development of a genetically and physically anchored EST resource for barley genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol"
199 c 173 g 87 t 3 others
                                                                                                                09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
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/clone_ib="Hordeum vulgare seedling green leaf EST
library HvCDNA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11194443.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 GACAACGACTCCAGTGGGCCGAGCAACGCGGGCGGG......GAGCT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GTCGTCGCCG.....CGGGAGCAGCACCCCTTCCTGCCCATCGCCAACG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 AspAlaLysGluThrIleGlnGluCysValSerGluTyrIleSerPheIl 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGlnGlnHi 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 sAlaAlaProAlaIleArgGluGlnAspArgLeuMetProIleAlaAsnV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 alileArgileMetArgArgValLeuProAlaHisAlaLysIleSerAsp 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 46.196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seq primer: ANTTANCCCTCACTAAAGGG
High quality sequence stop: 594.
Location/Qualifiers
                                                                                                              mRNA
                                                                                                            595 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: BF263449
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70.109
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US-09-435-054-2 x BF263449
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                                                                                                                                                                                                                                                                                                     Hordeum vulgare
                                                                                      seq_documentation_block:
LOCUS BF263449
536 TGCCTCCG 543
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                                                                                                                                    DEFINITION
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                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                          SOURCE
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BF263455 595 bp mRNA EST 09-MAR-2001
HV_CEa0006M16f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEa0006M16f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae, Triticeae; Hordeum.

1 (bases 1 to 595)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Wood, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for barley genomics
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11194449.
                                                                                                                                                                                                 97 hrAlaGluAspValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyr 113
                                                                                                                                                                                                                                                                                                                     114 ValGluProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAs 130
                                                                                                                                                                                                                                                                                                                                                164 ProvalSerGlyAlaAlaMetLeuProHisHisHisHisHisHspapme 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pAlaArgGlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 GAGG......GCGGNTCCCTNCACCACCACCACCGGTCAA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 spHisHisProHisSerMetSerProAlaAlaMetLeuLysSerArgGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......CTGCCCGAGATGCCAAGGAGCAACAATGC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 tGlnMetHisAlaAlaMetTyrGlyGlyThrAlaValProProAlaG 197
314 ACGCGACGACCTGCTCTGGGCAATGACCACCCTCGGCTTCGAGGACTAC
                                                                                      eThrGlyGluAlaAsnGluArgCysGlnArgGluGlnArgLysThr11eT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Seq primer: AATAAACCCTAAAGGG
High quality sequence stop: 590.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF263455.2 GI:13260837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est85:BF263455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         barley.
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/library HYCDNA0004 (Erysiphe infected & control)"
/library HYCLNA1011
/library HYCLNA11
/library HYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 GACAACGACTCCAGTGGGCCGAGCAACGCGGGCGGG......GAGCT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 ACGCCGACGACCTCCTCGCCATGACCACCCTCGGCTTCGAGGACTAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 ValGluProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAs 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pAlaArgGlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 GAGGGGGGG......TCCTCCACCACCACCACCACCGGAT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 spHisHisProHisSerMetSerProAlaAlaMetLeuLysSerArgGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 ProValSerGlyAlaAlaMetLeuProHisHisHisHisHisAspMe 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hrAlaGluAspValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 tGlnMetHisAlaAlaMetTyrGlyGlyThrAlaValProProAlaG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAlaAlaGlnGlnHi 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eThrGlyGluAlaAsnGluArgCysGlnArgGluGlnArgLysThrIleT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 sAlaAlaProAlaIleArgGluGlnAspArgLeuMetProIleAlaAsnV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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3.092
71.196
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US-09-435-054-2 x BF263455
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Ratio:
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                                                                                                                                                                                                                                                                                       BASE COUNT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wiridiplantae; Streptophyta; Eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases I to 561) Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu(Bazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
1. :561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="R2119e10R"
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/tissue_type="roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 GCCGAATCGCAAACCGGTGGTGGTGGTGGTGGAAGCCATGAGAGTGGCGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AAAATCGCTAAAGATGCTAAAGAGACTATGCAGGAATGTGTCTCTGAATT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 aAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgLeuMetP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 rollealaAsnValIleArgIleMetArgArgValLeuProAlaHisAla 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 rIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgGluGlnA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGlyGlyAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
cDNA clone RZ119e10R 5', mRNA sequence.
AV550943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Columbia"
                                                  AV550943.1 GI:8722356
                                                                                                                                                                                                                                                                                                                                                 Contact: Erika Asamizu
                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 c
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Ratio: 3.331
Percent Similarity: 83.448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AV550943
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ORGANISM
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MEDLINE
COMMENT
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                                ACCESSION
                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                             TITLE
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENCTH: 3395 base, pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-103-478-3
                                                                                                       (without alignments)
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Patent No. 5196516
Sequence 3, Appli
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                                                                                                                                                                Sequence 11, 7
Sequence 19, 7
Sequence 26, 7
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Sequence 1, 8
Sequence 1, 8
Sequence 1, 8
                                                                                          ; Search time 42.84 Seconds
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Sequence 3,
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Sequence 5,
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seg:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-764-233A-4
US-08-457-335A-6
US-08-729-214-6
US-09-028-934-6
US-08-764-233A-1
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US-09-320-878-19
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                                                                                                                                                                                                                                                       324599 seqs, 94655562 residues
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                                                                                       October 25, 2001, 10:49:35
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Maximum Match 100%
Listing first 45 summaries
                                                     OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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023070-077611US

NAME: Einhorn, Gregory P.
REGIESTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY AGENT INFORMATION:

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Sequence 1, Appli
Sequence 723, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5212296
Patent No. 5212296
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Sequence 10, Appl
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Lotan, Tamar
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
US-09-192-983-3

US-09-000-016-3

US-09-000-016-3

US-08-998-416-723

US-08-125-468-1

US-08-125-468-1

US-08-474-93-1

US-08-474-93-1

US-08-474-93-1

US-08-474-93-1

US-08-474-93-1

US-08-49-1

US-08-231-818-3

US-08-231-818-3

US-08-231-6468-1

US-08-2510-6468-1

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US-08-2510-6468-1
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Patent No. 6235975
 STATE: Calofornia COUNTRY: USA
RESULT 1
US-09-103-478-3
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STATE:
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                                                                                ggactccagcagcttcctccctgccgccggcggagaaatggctcggcggcgggggggcgc 130
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                                             Gaps
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Length 3395;
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APPLICANT: Lotan, Tamar
APPLICANT: Otto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
NUMBER OF SEQUENCES: 29
  Score 179; DB 4; Length 33:
Pred. No. 1.1e-27;
0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          023070-077611US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 38,440
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TELECOMMUNICATION INFORMATION:
      15.3%;
66.4%;
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MEDIUM TYPE: Floppy disk
  Ouery Match 15.39
Best Local Similarity 66.49
Matches 257; Conservative
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APPLICANT: Lotan, Tamar
APPLICANT: Lotan, Tamar
APPLICANT: Oldberg, Robert B.
APPLICANT: Fischer, Robert L.
AITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
NUMBER OF SEQUENCES: 29
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4766 TAACCGGTACCGTGAGATAGAGACCGA 4792
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FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 ccaccgctaccgcgagttcgagggcga 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09103478; Patent No. 6235975; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) US-09-103-478-4
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7560 base pairs
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.48
Matches 257; Conservative
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Teixeira De Mattos, Maarten J.
APPLICANT: Blom, Jolanda
TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF
TITLE OF INVENTION: MICRO-ORGANISMS AND MICRO-ORGANISMS OBFAINABLE BY SAID
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 ccggcgcggagaatggctcggcggcggcggcgccaacaatggcggcgctgctcagcagc 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 atgcggcggcggtggtcggcgagcaggaccggctgatgccgatcgcgaacgtgatccgca 216
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CURRENT APPLICATION NUMBER: US/09/319,989
                                                                                                                                                                                                                                                                                                                                                                                                /product= "LEC1"
                  APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/804,534
                                                                                                               NAME: EINDOR, GREGOLY P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0200
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09319989 Patent No. 6190914
                                                                                   FILING DATE: 21-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 68.13
Matches 246; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 1..627
; OTHER INFORMATION:
US-09-103-478-1
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear, MOLECULE TYPE: CDNA
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US-09-319-989-3
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119 ggcgggggggggcaacaatggcggcgctgctcagcagcatgcggcggcggcgatccggga 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 gcaggaccggctgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggc 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 gcacgccaagatctcggacgacgccaaggagacgatccaggagtgcgtgtcggagtacat 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 cagcttcatcaògggggaggccaacgagcggtgccagcgggagcagcagcatcac 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: DNA construct OTHER INFORMATION: encoding HAP3
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.7%; Score 78.4; DB 4; Length 835; Best Local Similarity 53.2%; Pred. No. 1.2e-07; Matches 166; Conservative 0; Mismatches 146; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: PCT/NL97/00688
EARLIER FILING DATE: 1997-12-12
EARLIER APPLICATION NUMBER: EPO 96203520
EARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/07977434 Patent No. 5466591
                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (201)..(632)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey ZIP: 07110-1199
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                                                                                                                                                                   LENGTH: 835
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                                                                                                                                             SEQ ID NO 3
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FILING DATE

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us-09-435-054-1.rni

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                                                                                                1154 ccgaggggggggcccggcggracgggggggggggaggaggaggacgccgccccgggccc 1213
                                                                                                                                                                                                                                                                                                                                                                                                      1214 TCCTTTCGGAAAGGCTCTGGCAGGCCCTTTACCCCCGGGTGGCGGGGGGAGGAAAGGCTCC 1273
                                                                                                                                                                                                                                                    cgggggaggccaacgagcggtgccagcgggagcagcgagaccatcaccgccgaggacg 369
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                                                 190 tgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgcacgccaaga 249
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Patent No. 5795762
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-JUN-1995
CLASSIFFTANTON
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CORRESSONDERGE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,434
FILING DATE: 23-FEB-1993
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
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FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
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28-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER: 1
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45.1%; Pred. No. 4.8e-05;
tive 0; Mismatches 294; Indels 0)
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510).814-2972
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 56,471
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 55,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                     PRIOR APPLICATION DAME:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
FILING DATE: 28-5EP-1990
PRIOR APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
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ORGANISM: Thermus species sps17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
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FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 590,490
FILING DATE: 28-5EP-1990
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 523,394 FILING DATE: 15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Luann Cserr
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2493 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
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US-07-977-434-5
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130 ccaacaatggcggcgctgctcagcagcatgcggcggcggcgatccgcggagcaggaccggc 189
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45.1%; Pred. No. 4.8e-05;
tive 0; Mismatches 294; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5795762 8753
                                                                                                                                                                APPLICATION NUMBER: WO PCT/US90/07641.
FILING DATE: 21-DEC-1990.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: Case No. TELEOOMNULICATION: TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                             FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455.611
FILING DATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Thermus species sps17
                APPLICATION NUMBER: US 063,509 FILING DATE: 17-JUN-1987 PRIOR APPLICATION, DATA:
                                                                                                              APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                   US 899, 241
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                   22-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2493 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                              APPLICATION NUMBER:
FILING DATE: 22-AUG
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; LOCATION: 1..2
US-08-458-819-5
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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1214 TCCTTTCGGAAAGGCTCTGGCAGGCCCTTTACCCCCGGGTGGCGGAGGAGGAAGGCTCC 1273
                                                                                                                       1274 TITGGCTCTACCGGGAGGTGGAGCGCCCCTCGCCCAGGTCCTCGCCCACATGGAGGCCA 1333
                                       1394 TGGAGCGCTCGAGGCCGACCGCTGGCGGCCACCCCTTCAACCTGAAC 1449
                                                                                                                                                                                                        550 cccgcgggccagtctccggagccgccatgctaccgcaccaccaccaccacgac 605
                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application PC/TUS9107035
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: 1'THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FILING DATE: 19910930
CLASSIFICATION: 435
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APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1400 Fifty-third Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US 143,441
12-JAN-1988
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22-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cetus Corporation
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-SEP-1990
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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FILING DATE: 22-DEC
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California
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STATE: Car.
94608
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PRIOR APPLICATION DATA:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 cgggggaggccaacgagcggtgccagcgggagcagcgcaagaccatcaccgccgaggacg 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 ccccatcgcgcggcggcgaccaccaccgcactccatgtcgccagcggcgatgctcaagt 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 tgatgccgatcgcgaacgtgatccgcatcatgcggcgcgtgctgccggcgcacgccaaga 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 teteggaegaegaegaegagaegaeccaggagtgegtgteggagtaeateagetteatea 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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45.1%; Pred. No. 4.8e-05;
ive 0; Mismatches 294; Indels 0
                                                                                                                                                                                                                                                                                                                          NAME: Sias Ph.D, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: Case No. 2580
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-420-3300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2493 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
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                                                                                                                                                    APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 609,157
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Matches 242; Conservative
                                                         02-NOV-1990
                                                         FILING DATE: 02-NOV-1 PRIOR APPLICATION DATA:
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ORGANISM: The
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; LOCATION:
PCT-US91-07035-5
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16476 CTCCCTCGAGGACGCGGGCCCGCATCGCCGCCCTGCGCAGCAAAGCGTCACCACCACGTCGCC 16535
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Pred. No. 0.0056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261B
FILING DATE: 08-JUN-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 170;
                                                                                                                                             APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36,129
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELERAX: 919-541-8689
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Best Local Similarity 48.2%;
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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US-08-258-261B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                 10532
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                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                         STATE:
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Sequence 6, Application US/08258261B Patent No. 5639949

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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligon, James M.
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STRANDEDNESS: single
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ZIP: 10532
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Db 16596 CIGGGCCGACAGGCTCTCCATCGCCGCCGTCAACAGCCCCCAGGGCCACGCTCGTATCCGG 16655
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48.2%; Pred. No. 0.0056;
tive 0; Mismatches·170; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances TIMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
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                                                                   Db 16656 CGAGCCGCCGCCGACGACGCTGATC 16683
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FILING DATE: 01-JUN-1995
CLASSIFICATION: 4355
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATORNEY/AGENT INFORMATION:
NAME: ELMC: James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
                                        656 cgggcctccccaccacggggttcctc 683
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James MarbicanT: Beck, James Joseph
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    US-08-456-837-6; Sequence 6, Application US/08456837; Patent No. 5643774
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TELEFAX: 919-541-8689
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 7 Skyline Drive
Hawthorne
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Best Local Similarity
Matches 158; Conserva
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HYPOTHETICAL: 1
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16476 CTCCCTCGAGGACGCGGCCCGCATCGCCGCCCTGCGCAAAAGCGTCACCACCGTCGCC 16535
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT IRFORMATION:
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APPLICANT: BCK, James Joseph
APPLICANT: Ryals, John Andrew
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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7 Skyline Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5662898
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MOLECULE TYPE:
HYPOTHETICAL: N
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REGISTRATION NUMBER: 36,129

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                                                                                                                    Gaps
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                                                                         Query Match 4.8%; Score 56; DB 1; Length 28958; Best Local Similarity 48.2%; Pred. No. 0.0056; Matches 158; Conservative 0; Mismatches 170; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
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APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
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Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
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CORRESPONDENCE ADDRESS:
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APPLICANT: Schupp,
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APPLICANT:
APPLICANT:
APPLICANT:
; ANTI-SENSE:
US-08-457-342-6
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US-08-457-646A-6
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16596 CTGGGGCGACAGGCTCTCCATCGCCGCCGTCAACAGCCCCAGGGCCACGCTCGTATCGGG 16655
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Pred. No. 0.0056;
0; Mismatches 170; Indels
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APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
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Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.8%;
Best Local Similarity 48.2%;
Matches 158; Conservative
                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                          linear
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US-08-457-335A-6
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Query Match

Goral Similarity 48.2%; Pred. No. 0.0056;

Matches 158; Conservative 0; Mismatches 170; Indels
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TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
NUMBER OF SEQUENCES: 10
SOFTWARE: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,076A
FILING DATE: U1-JUN-1995
PRIOR APPLICATION: 435
ADDITE: U1-200-1995
                                                                                                                                                                                                                                                                                                                                 CGC 1506/CIP3
                                                                                                                                                            PRIOR APPLICATION 1913

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-UN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Un-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CI
TELECHONICATION INFORMATION:
TELECHONE: 919-541-8619
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
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MOLECULE TYPE: DNA (genomic)
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Schupp, Thomas
Beck, James J.
Hill, Dwight S.
Neff, Snezanna
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APPLICANT: Ligon,
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US-08-458-076A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-764-233A-4
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APPLICANT:
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16416 CGCCGCCGTCGTCGCCACAGCCAGAGATAGCCGCCCTTCGTCGCAGGCGCTCT 16475
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4.8%; Score 56; DB 1; Length 28958;
Best Local Similarity 48.2%; Pred. No. 0.0056;
Matches 158; Conservative 0; Mismatches 170; Indels
                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,41
REFERENCE/DOCKET NUMBER: 1506/CIP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/764,233A
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                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-0CT-1996
                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Sorangium cellulosum IMMEDIATE SOURCE:
                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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STRANDEDNESS: sing
          STREET: 520
TTTY: Tarrytown
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                 FILING DATE
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                                                                                COUNTRY:
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Db 16596 CTGGGGCGACAGGCTCTCCATCGCCGCCGTCAACAGCCCCAGGGCCACGCTCGTATCCGG 16655
                                      Db 16656 cgAgcccgccgccgrcarcgacgcgrgArc 16683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/729,214
                                                                                                                                                                                                                                                               Sequence 6, Application US/08729214 Patent No. 5817502
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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TYPE: nucleic acid
STRANDEDNESS: single
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 48.28
Matches 158; Conservative
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US-08-729-214-6
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48.2%; Pred. No. 0.0056;
tive 0; Mismatches 170; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                            APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: antipathogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET, NUMBER: 36,129
REFERENCE/DOCKET, NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
FORMATION FOR PARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/457,335A FILING DATE: 01-JUN-1995 CLASSIFICATION: 800
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APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-0N0-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-0nn-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                     Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
Lam, Stephen Ting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 6, Application US/08457335A
Patent No. 5723759
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                 Schupp, Thomas
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Best Local Similarity 48.28
Matches 158; Conservative
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-08-457-335A-6
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APPLICANT:
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Db 16356 CGCCCTCTTTGCCGTCATGGTCTCCCTGGCCCCTCTGGCGCTCGCCTCGGCGTCGAGCC 16415
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18.2%; Pred. No. 0.0056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGC 1506/CIP5
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- Db 16476 CTCCCTCGAGGACGCGCCGCATCGCCGCCTGCGCAAGCGTCACCACCGTCGCC 16535
- Oy 536 ggcgatgctcaagtcccggggccagtctccggagccatgctaccgcaccacca 595

  Db 16536 GGCAACGGGCATGGCCGCCGTCGGCGCTCCGACCTCCAGACCTCCTCC 16595
- Oy 596 ccaccacgacatgcaggtgcacgccatgtacgggggaacggccgtgccccggcggc 655

  Db 16596 CTGGGGCGACAGGCTCTCCATCGCCGCGTCAACAGCCCCAGGCCACGCTCGTATCCG 16655
- Oy 656 cgggctctcaccacggcgggttcctc 683

Search completed: October 25, 2001, 12:01:59 Job time: 4344 sec

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                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-478-1
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US-09-435-054-2 x US-09-103-478-1
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPX -WAIT -THREADS=1
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                                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
               out_format : pfs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sec): 38.160000
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                                                       Date: Oct 25, 2001 2:25 PM
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Database length: 94655562
Search time (sec): 38.16000
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Query: US-09-435-054-2
                                                                                                                                                                              Command line parameters:
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APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-aki
APPLICANT: Ohto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             023070-077611US
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APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..627
OTHER INFORMATION: /product- "LEC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/103,478
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 1, Application US/09103478
Patent No. 6235975
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38,440
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REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0200
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nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    San Francisco
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Percent Identity: 46.988

Length:

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APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-ak, Robert
APPLICANT: Gldberg, Robert B.
APPLICANT: Fischer, Robert L.
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
CORRESPONDENCE: 29
CORRESPONDENCE ADDRESS:
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                                                                                                              72 ATGTGTGGCTCGTGAGCAAGACCAATACATGCCAATCGCAAACGTCATAA 121
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22 GCCGGCGCCGGTGACAACAATGGTATCGTGGTCCAGCAGCAACCACC 71
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    Sequence 3, Application US/09103478
    Patent No. 6235975
    Patent No. GassAps
    APPLICANT: Harada, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 ProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaAr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 yGluAlaAsnGluArgCysGlnArgGluGlnArgLysThrIleThrAlaG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 LysGluThrIleGlnGluCysValSerGluTyrIleSerPheIleThrGl 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 aProAlaIleArgGluGlnAspArgLeuMetProIleAlaAsnValIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 SeralaalaGlyGlyAlaAsnAsnGlyGlyAlaalaGlnGlnHisAlaAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 46.988
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NDATA:
APPLICATION WHERE: US/09/103,478
FILING DATE: 24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-103-478-3 from: 1 to: 3395
ADDRESSEE: Townsend and Townsend and Crew LLP
                 Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-435-054-2 x US-09-103-478-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3395 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494.00
                                        San Francisco
Calofornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                  COUNTRY:
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REFERENCE/DOCKET NUMBER: 023070-077611US TELECOMMUTICATION INPORMATION: TELEPHONE: (415) 576-0200 INPORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 7560 base pairs TYPE: nucleic acid STRANDENESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	<pre>ignment_scores:     Quality: 494.00</pre>	gnment_ -09-435	ign se 16	COGGCGCCGGTGACAAGAACAATGGTATCGTGGTCCAGCAGCAACCACC	32 aProalaIleargGluGlnaspargLeuMetProIlealaAsnValIlea 49 :::	49 rglleMctArgargValLeuProAl#HisAlaLysIleSerAspaspala 65	66 LysGluThrIleGlnGluCysValSerGluTyrIleSerPhe leThrGl 82	82 yGlualaasnGluargCysGlnargGluGlnargLysThrIleThralaG 99 	99 luAspValLeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValGlu 115      :::	116 ProLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaAr 132	132 gGlyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisH 149      :::    4796 TGGTTCTGCACTTAGAGGT	oval 165	4815	166 SerGlyAlaAlaMetLeuProHisHisHisHisHisHisAspMetGlnMe 182	4838 4838	Pr	OHISHISGlyGlyPheLeuMetProHisProGlnGlySerSerHisTvr 215	
	nment_ cent S	1.0	gn se 16	449	32	49 549	669 599	82 649	669	116	132 g       796 T	49 isProHi	815	66 SerGlyAl	838	182 tHisAlaAl	9 roHisHisG	

6850

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GENERAL INFORMATION:

APPLICANT: Grivell, Leslie A.

APPLICANT: Grivell, Leslie A.

APPLICANT: Teixeira De Mattos, Maarten J.

APPLICANT: Teixeira De Mattos, Maarten J.

APPLICANT: Teixeira De Mattos, Maarten J.

TITLE OF INVENTION: METHODS

TITLE OF INVENTION WHERE: US/09/319,989

CURRENT FILING DATE: 1999-06-12-12

EARLIER FILING DATE: 1999-06-12-12

EARLIER FILING DATE: 1996-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: DNA construct OTHER INFORMATION: encoding HAP3
                                                                              4881 CTACCTCCGGGTCCTTATGGTTAT......GGTATGTT 4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 sAlaMetAlaAlaTyrTyrGlyGlyAlaAlaTyrAlaProGlyAsnGlyG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 CCAGAGGATACTCAGGAGAACGGT......GGAAACGCTAGCTCCAG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 GGCTACCCATCAACAATGTAGCGCGACTCATGAAGAATACTCTCCCACCG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 HisAlaLysIleSerAspAspAlaLysGluThrIleGInGluCysValSe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 euMetProIleAlaAsnValIleArgIleMetArgArgValLeuProAla 57
                                                                                                                                                                                  4963 CGTCGGGTCAAGATGAATCCAGTGTTGGTGGTGGTCTTTCGTTTTC 5009
                                                                                                                                               245 lyserGlyAspGlySerGlySerGlyGlyGlyGlyGlyGlySerAlaSer 260
                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-319-989-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 2
Percent Identity: 50.420
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US-09-435-054-2 x US-09-319-989-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
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Quality: 295.50
Ratio: 3.283
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US-09-319-989-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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136 uValProGlyAlaAlaProSer...ArgGlyGlyAspHisHisProHisS 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 CGAGACGCTGCTGCCGGCGGGCGCGTGGCGGCGGTGGACATCGCCG 116
                                                                                                                                             108 LeuGlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuH18ArgTy 124
91 luGlnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerArg 107
                                                                                   472 ACAAAAGAAAAAGACGATAAACGGGGAAGACATTCTCATATCATTGCACGCC 521
                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-758-662-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 35.503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUBBE: US/08/758,662 FILING DATE: 29-NOV-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-758-662-4 from: 1 to: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: No. 611450tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REPERENCE/DOCKET NUMBER: 390036.402C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08758662
Patent No. 6114150
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-435-054-2 x US-08-758-662-4
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weissman, Sherman
APPLICANT: Baskaran, Namadev
TITLE OF INVENTION: AMPLIFICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 167.50
Ratio: 1.971
nilarity: 50.296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                     124 rArgGlu 126
                                                                                                                                                                                                                                                             572 CAGGCAA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98104
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167 ATGAACAGCGTGCCGTGCACTTCCACGT...GCCTCTGGCGCA 213
                                                                               169 AlaMetLeuPro.HisHisHisHisHisAspMetGlnMetHisAlaA 185
                                                                                                         202 GlyGlyPheLeuMetProHisProGlnGlySerSerHisTyrLeuProTy 218
                                                                                                                                                               185 laMetTyrGlyGlyThrAlaValProProProAlaGlyProProHisHis 201
                                                                                                                                                                                                      243 CGCTC.....GAA 250
                                                                                                                                                                                                                                                                                                                              218 rAlaTyrGluProThrTyrGlyGlyGluHisAlaMetAlaAlaTyrTyrG 235
                                                                                                                                                                                                                                                                                                                                                                     289 cececrcareccececececececececece 335
                                                                                                                                                                                                                                                                                                                                                                                                                                      258 rAlaSerHisThrProGlnGlySer.....GlyGlyLeuGluHisProH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 .....GlyGlySerGlyAspGlySerGlySerGlyGlyGlyGlyGlySe 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-845-998-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
    Sequence 7, Application US/08845998
    Fatent No. 5879892;
    Fatent No. 5879892;
    Fatent No. 5879892;
    FAPLICANT: Van Baren, Nicolas
    APPLICANT: Coulie, Pierre G.
    APPLICANT: Ducas, Sophie
    APPLICANT: Boon, Thierry
    TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
    NUMBER OF SEQUENCES: 16
    CORRESPONDENCE ADDRESS:
    ADDRESS:
    ADDRESS:
    STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                              235 lyGlyAlaAlaTyrAlaProGlyAsn.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
RECISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPHONE: (617)720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 ACCCG 490
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125 ArgGluPheGluGlyAspAlaArgGlyValGly.....Le 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 uValProGlyAlaAlaProSer...ArgGlyGlyAspHisHisProHisS 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 AlaMetLeuPro.HisHisHisHisHisApMetGlnMetHisAlaA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GlyGlyPheLeuMetProHisProGlnGlySerSerHisTyrLeuProTy 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 laMetTyrGlyGlyThrAlaValProProProAlaGlyProProHisHis 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 CCCGGCGATCTGCTGGACCACATCTCCTCGCCGTCG......CT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 ralaTyrGluProThrTyrGlyGlyGluHisAlaMetAlaAlaTyrTyrG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 CGCGCTCATGGCCGGCGCGGCGCGCGCGCCC...GCGGCCGGCGG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 lyGlyAlaAlaTyrAlaProGlyAsn.....
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                                                                                                                                                                                                                                                                 Length: 169
Gaps: 11
Percent Identity: 35.503
                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-845-998-7 from: 1 to: 4524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
   Sequence 7, Application US/09206537
                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-435-054-2 x US-08-845-998-7
                                LENGTH: 4524 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             167.50
1.971
50.296
                                                                                                                                                                              174..1433
                                                                                 linear
                                                                                                                S
                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                               ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 isPro 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              745 ACCCG 749
                                                                               TOPOLOGY:
                                                                                                                                                                              ; LOCATION:
US-08-845-998-7
                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                               alignment_scores
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136 uValProGlyAlaAlaProSer...ArgGlyGlyAspHisHisProHisS 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AlaMetLeuPro.HisHisHisHisHisAspMetGlnMetHisAlaA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaps: 11
Percent Identity: 35.503
                                                                                                                                                                                                                                                                  MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 4524
                                                                  APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
TUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                              ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMUNICATION INFORMATION:
TELECAX: (617)720-3500
TELEFAX: (617)720-341
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
LENGTH: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-206-537-7 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
           Van Baren, Nicolas
Coulie, Pierre G.
De Smet, Charles
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US-09-435-054-2 x US-09-206-537-7
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Quality: 167.50
Ratio: 1.971
Percent Similarity: 50.296
                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
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GENERAL INFORMATION:
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                                   APPLICANT:
APPLICANT:
                 APPLICANT:
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STATE:
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APPLICANT: Vance, Jeffrey M.
APPLICANT: Enghild, Jan
APPLICANT: Enghild, Jan
APPLICANT: Enghild, Jan
APPLICANT: Enghild, Jan
APPLICANT: Strittmatter, Warren J.
TITLE OF INVENTION: Therapeutics for Diseases Associated
TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion
NUMBER OF SEQUENCES:
ADDRESSE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte STREET: ADARDESS:
STREET: No. 5723301th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 .....GlyGlySerGlyAspGlySerGlySerGlyGlyGlyGlyGlySe 258
                                                                                                                                                                                          510 CCCGGCGATCTGCTGGACCACATCTCCTCGCCGTCG......CT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 rAlaSerHisThrProGlnGlySer.....GlyGlyLeuGluHisProH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695 CGCGGGCGCGCGGCGGGCTCCTGGGCGCTCCGCGCACCCTC 744
                                                                                                                                                       202 GlyGlyPheLeuMetProHisProGlnGlySerSerHisTyrLeuProTy 218
                                                                                                                                                                                                                                                              21.8 ralaTyrGluProThrTyrGlyGlyGluHisAlaMetAlaAlaTyrTyrG 235
                                                                                                                                                                                                                                                                                                                  185 laMetTyrGlyGlyThrAlaValProProProAlaGlyProProHisHis 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-553-110-2
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473 .....ccaccaccaccaccaccac
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 31,665
REFRENCE/DOCKET NUMBER: 5405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08553110
Patent No. 5723301
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APPLICANT: Burke, James R.
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LENGTH: 1853 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                         502 CGCTC.....
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1185 ACCAGTCTCA.....ACACATCACCATCACCACCAGCAAC 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 yProValSerGlyAlaAlaMetLeuProHisHisHisHisHisAspM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 AlaValProProPlaGlyProProHisHisGlyGlyPheLeuMetPr 207
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    Sequence 22, Application US/09041886
    Patent No. 6235872
    GENERAL INFORMATION:
    APPLICANT: Bracesen, Dale E.
    APPLICANT: Rabizadeh, Sharroz
    TITLE OF INVENTION: Proapoptotic Peptides, Dependence;
    TITLE OF INVENTION: Proapoptotic Peptides of Use
    NUMBER OF SEQUENCES: 72
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-041-886-22
                                                                                                                                                                                                                                                                                                                        Percent Identity: 31.690
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1493 CCTACCCATGTTCACACCCCTCCCCT 1518
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US-09-435-054-2 x US-08-553-110-2
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1.934
53.521
         peptide
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                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
; MOLECULE TYPE:
US-08-553-110-2
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1610 CATCCAGGCCCCTTCCCTCCTTACTGGGGCCCCAGTCCACCGCCCACC 1659
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Percent Identity: 31.690
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
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                                RILLING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4279 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-041-886-22
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US-09-435-054-2 x US-09-041-886-22
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 1.934
Percent Similarity: 53.521
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Ratio: 1.934
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239..3794
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US-09-041-886-22
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us-09-435-054-2.p2n.rni

hralavalpropropio	73 shishishishishaspMetGlnMetHisAlaAlaMetTyrGlyGlyT 19 	41 euMetProlleAlaAsnVallleArgileMetArgArgValLeuProAla 57 ::::         :::::     ::::	24 yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	B ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24 	435-054- seg 1/1	NUMBER OF ENVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTAS: NUMBER OF SEQUENCES: 24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/315,316 APLICATION DATE: 24-FEB-1989 ID NO:1: LENGTH: 2176	atent No. 5320958 APPLICANT: INOUYE, SUNIKO;HSU, MEI-YIN;EAGLE, SUSAN; NOUYE, MASAYORI
173 SHISHISHISHISHSASPMELGINMELHISALAAlaAlaMETTyrGlyGlyT 190		### ### ##############################	eumetprollealaasnvallleargllemetargargvalLeuproala 57	y yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	ProAlaalaGlyAlaGluAsnGlySerAlaalaGlyGlyAlaaAsnAsnGl 24	Dength: 296	LE OF INDERTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTAN BERN PADLICATION DATA:  REWIT APPLICATION NOMBER: . US/O7/315,316  FILING DATE: 24-FEB-1989  NO:1:  LUCATION NUMBER: . US/O7/315,316  ENGTH: 2176  LENGTH:
158 MetLeuLysSerArgGlyProValSerGlyAlaAlaMetLeuProHi 173	158 MetLeuLysSerArgGlyProValSerGlyAlaAlaMetLeuProHi 173         :::::	### HisalaLysileSerAspapalaLysGluThrileGlnGluCysValse 74	eumetProllealaasnvallleargllemetArgargValLeuProala 57	y yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	ProAlaalaGlyAlaGluAsnGlySerAlaalaGlyGlyAlaaAsnAsnGl 24	Length: 296	TILE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTAS;  MARERA PALICATION DATA:  APPLICATION NUMBER: US/07/315,316  FILING DATE: 24-FEB-1989  NO:1:  LENGTH: 2176  1-1  CADA: 1.072  Ratio: 1.073  Ratio: 1.072  Ratio: 1.073  Ratio: 1.072  Ratio: 1.073  Ratio: 1.073
141 laProSerArgGLyGlyAspHisHisProHisSerMetSerProAlaAla 157	141 laProSerArgGLyGlyAspHisHisProHisSerMetSerProAlaAla 157	### HisalaLysileSerAspaspalaLysGluThrileGinGluCysValse 74	eumetprollealaasnvallleargllemetargargValLeuproala 57	y yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24	int_scores:  Quality: 141.50  Ratio: 1.072  Ratio: 1.072  Ratio: 1.072  Ratio: 1.072  Ratio: 1.072  It Similarity: 44.595  Percent Identity: 24.324  Int_block:	THE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASINGER APPLICATION DATA:  APPLICATION DATA:  APPLICATION NUMBER: US/07/315,316  FILING DATE: 24-FEB-1989  NO.1:  LENGTH: 2176  JUN01:  LENGTH: 2176  LENGTH:
4 rArgGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAlaA 141  ::::::::::::::!	4 rArgGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAlaA 141  ::::::::::::::::::::::::::::::::::	### HisAlaLys1leSerAspaspalaLysGluThrileGlnGluCysValse 74	eumetprollealaasnvallleargllemetargargvalLeuproala 57	y yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24	Int_scores:  Quality: 141.50  Ratio: 1.072  Record Common of the common	THE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTAS;  MRBERO CS SEQUENCES: 24  APPLICATION DATA:  APPLICATION NUMBER: US/07/315,316  FILING DATE: 24-FEB-1989  LENGTH: 2176  LENGT
B LeuGlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTy 124  1	B LeuGlyPheAspAspTyrValGluProLeuGlyAlaTyrLeuHisArgTy 124  3	B HisalaLysileSerAspaspalaLysGluThrileGlnGluCysValse 74          :::     :::       CACGCACTACGTGCACGACGGACGGCACCGCACCGCAGCGCA 122	eumetProllealaasnValllearglleMetArgargValLeuProala 57	4 yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24	Tength: 296   Ratio: 1.072   Ratio: 1.072   Gaps: 9     Tello: 1.072   Ga	The OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASINGREW APPLICATION DATE:   APPLICATION DATE: 24-FEB-1989   Length: 296   Gaps: 24-FEB-1989   Length: 2176   Length: 2176   Gaps: 24-FEB-1989   Length: 2176
luGinArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerarg 107	luGinArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerarg 107	B HisalaLysileSerAspAsPAlaLysGluThrileGlnGluCysValse 74	eumetProllealaasnValllearglleMetArgargValLeuProAla 57	4 yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAspArgL 41	ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24	December	The OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASINGRE OF SEQUENCES: 24   RREM.   APPLICATION DATA:   APPLICATION NUMBER: US/07/315,316   FILING DATE: 24-FEB-1989   STILING DATE: 24-FEB-1989   Caps: 1.072   Caps: 1.073   Caps: 1.074   Caps: 1.072   Caps: 1.076   Caps: 1.0
### ##################################	# rGluTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArgG 91 # :::   :::::   ::::    # cGATTACGTCCCCAAGCTGGGTGGGGGGGGGGGGGGGGGG		41 eumetProllealaasnVallieargilemetArgargValLeuProala 57 ::::       ::::        :::         :::             :::	24 yGlyAlaAlaGlnGlnHisAlaAlaProAlaIleArgGluGlnAsPArgL 41	B ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24	December	The OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTAS;   MBBER OF SEQUENCES: 24
seg 1/1 to: 5320958-1 seg 1/1 to: 5320958-1 seg 1/1 to: 5320958-1 seg 1/1 to: 5320958-1 lli::::::::::::::::::::::::::::::::	seg 1/1 to: 5320958-1 lll::: lll::: lll:::: lll:::: lll:::: lll:::: ll ::: ll ::: ll :: ll :	<pre>nt_block:</pre>	<pre>nt_block: -435-054-2 x 5320958-1 seg 1/1 to: 5320958-1 from: 1 to: 2176  ProAlaAlaGlyAlaGluAsnGlySerAlaAlaGlyGlyAlaAsnAsnGl 24            ::    ::    ::             </pre>	nt_block: 435-054-2 x 5320958-1 seg 1/1 to: 5320958-1 from: 1 to: 217			LE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTAS; BER OF SEQUENCES: 24 RENT APPLICATION DATA: PPLICATION WURBER: US/07/315,316 ILING DATE: 24-FEB-1989 NO.1: ENGTH: 2176

```
1713 CAAGCCGCGCGCACGCACGTCCCCCGGTGCCGCTGTTTCCCC 1762
1563 GCCCCAGGGCGCCCCACGTCGCCGGCATCACCAACGCGCTGTGCCTGA 1612
                                                                            .613 AGCTGGACAAGCGGCTGTCGCGCTCGCGAAGCGGCTGGGCTTCACGTAC 1662
                                                                                                                                    216 euProTyrAlaTyrGluProThrTyrGlyGlyGluHisAlaMetAlaAla 232
                                                                                                                                                                                                                        233 TyrTyrGlyGlyAlaAlaTyrAlaProGlyAsnGlyGlySerGlyAspGl 249
                                            207 oHisProGlnGlySer.....SerHisTyrL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-041-886-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 312
Gaps: 15
Percent Identity: 23.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                             1813 CGCGTGGCGCGCAAGGGCACGGGCAGCGGGTGACGG 1850
                                                                                                                                                                                                                                                                                                                                                                                                      257 .....GlySerAlaSerHisThrProGlnGlySerGly 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9049
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3715 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136.50
0.968
45.192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532..3286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-041-886-10
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lignment_block: US-09-435-054-2	_block:  5-054-2 x US-09-041-886-10	
Align seg 1/1	g 1/1 to: US-09-041-886-10 from: 1 to: 3715	
8 1257	0	24 1306
24	yGlyalaalaGlnGlnHisAlaalaProAlaIleArgGluGlnAspArg	40 1347
41		52 1397
53 1398	ArgValLeuProal 	57 1447
57	aHisAlaLysIleSerAspAspAlaLysGluThrIleGluGysValS ::::::::::::::::::::::::::::::::::::	74 1497
74	erGluTyrIleSerPheIleThrGlyGluAlaAsnGluArgCysGlnArg :::      ::    GGCAGCGCTGCAGGAGG	90 151 <b>4</b>
91	GluGlnArgLysThrIleThrAlaGluAspValLeuTrpAlaMetSerAr 	107 1538
107	gLeuGlyPheAspAspTyrValGluProLeuGlyAlaTyr.LeuHisArg :::        :::	123 1554
124	TyrArgGluPheGluGlyAspAlaArgGlyValGlyLeuValProGlyAl	140 1580
140	aalaproserargGlyGlyaspHisHis	149 1630
150	GACCGCCCCCTCCGCCGCCTCCCATCCCCACGCTCGC	158 1671
159 1672		172
172 1722	OHISHISHISHISHISHSASPMEtGlnMetHisAlaAlaMetTyrGlyG::::::::::::::::::::::::::::::::::	189 1762
189	1yThralaValProProProAlaGlyProProHisHisGlyGlyPheLeu ::	205 1806
206	MetProHisProGlnGlySerSerHisTyrLeuProTyrAla	219 1844
220	TyrGluProThrTyrGlyGlyGluHisAlaMetAlaAlaTyrT 	234 1875
234	yrGlyGlyAlaAlaTyrAlaProGlyAsnGlyGlySerGlyAspGlySer         :::::::::::::::::::::::::::::	250 1923

```
GENERAL INFORMATION:

APPLICANT: Dahlbrey, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVENSTOCK, MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: Californies
COUNTRY: United States of America
ZIP: 94104
COUNTRY: United States of America
ZIP: 94104
COUNTRY: United States of America
SIPPRES: Floppy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/073,384C
FILING DATE: 04-JUN-1993
CLASSIFICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INPORMATION:
NAMME: CARTOLL DATE G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 leargGluGlnAspArgLeuMetProlleAlaAsnVallleArglleMet 51 ::||||||| :::
                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-073-384C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 17
Percent Identity: 26.498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-073-384C-2 from: 1 to: 2496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                1974 CACTCGGCCCCTCAGGGGCTGGCGGCCAGGA 2007
                                                                                                   260 .SerHisThrProGlnGlySerGlyGlyLeuGlu 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FORS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                              seq_documentation_block:
    Sequence 2, Application US/08073384C
    Patent No. 5541311
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-435-054-2 x US-08-073-384C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: DNA (genomic) US-08-073-384C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2496 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.934
45.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 134.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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107	9 TGCGGGAGGGCCTGGACCTCTTCCCAGAGGACGACCCCCATGCTCCTG	1125
S	ArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysGluTh	89
1126		1154
115	8 rIleGlnGluCysValSerGluTyrIleSerPheileThrGlyGluAlaA   :::       :::       ::         ::           ::	85 1204
1205	5 snGluargCysGlnargGluGlnargLysThrIleThralaGluaspVal 1 ::	.01
102	2 LeuTrpAlaMetSerArgLeuGlyPheAspAspTyrValGluPr 1	.16
116	6 oLeuGlyalaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgG 1	33
133	3 lyvalGlyLeuValProGlyAlaAlaAroSerArgGlyGlyAspHisHis 1 	49
150	ProHisSerMetSerProAlaAlaMetLeuLysSerArgGlyProVal	65 444
166	ACCTCAAC	71
172	YProHisHisHisHisHisAspMetGlnMctHisAlaAla 1	85 544
186 1545	MetTy	02 585
202	yGlyPheLeuMetProHisProGlnGlySerS 2	13 623
213	erHisTyr ::    AACACCTACATAG	15 673
216 1674	LeuProTyralaTyrGluProThrTyrGlyGlyGluHisAlaMetAla 2	31 720
232	AladyrTyrGlyGlyA	7
23	LaAlaTyralaPro	49
250 1821	CTTGGACTACAGCCAGATTGAGCTTCGGGTCCTGGCCCACCTCTCGGGG	00 1
258	ralaSerHisThrProGlnGlySerGlyGlyLeuGluHisProHisPro 27 : :::	4 T
g_name	: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-254-359A-2	

seq\_documentation\_block:

APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS: 19 GlyGlyAlaAsnAsnGlyGlyAlaAlaGln.GlnHisAlaAlaProAlaI 35 35 leArgGluGlnAspArgLeuMetProIleAlaAsnValIleArgIleMet 51 52 ArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysGluTh 68 68 rIleGlnGluCysValSerGluTyrIleSerPheIleThrGlyGluAlaA 85 COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A Gaps: 17 Percent Identity: 26.498 Align seg 1/1 to: US-08-254-359A-2 from: 1 to: 2496 ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 STATE: CALIFORNIA FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-UUN-1993
PRIOR APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATPOINEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
TREGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 2:
FELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2496 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-254-359A-2 Sequence 2, Application US/08254359A Patent No. 5614402 GENERAL INFORMATION: alignment\_block: US-09-435-054-2 x US-08-254-359A-2 Quality: 134.50 Ratio: 0.934 Percent Similarity: 45.426 alignment\_scores:

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                                                                                                                                                                                                                                                                                                                                                              1205 GGGAGAGGCCCTCCTGGCCGAGCGCCTCTTCCAGACCCTAAAGGAGGGCGC 1254
                                                                                                                                                            1255 CTTAAGGGAGAAGAACGCCTGCTTTGGCTTTACGAGAGGTGGAGAAGCC 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1545 TGCCGTGCTGCTTGCTGCTGCGAGGCCCACCCATCGTGG 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1401 CCA.....GCTGGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCA 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1445 ACCICAACICCCGCGACCAGCTGGAGCGGGTGCTCTTTGACGAGCTGGGC 1494
                                                                                                      102 LeuTrpAlaMetSerArgLeu.....GlyPheAspAspTyrValGluPr 116
                                                                                                                                                                                                                                                                                                                         133 lyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHis 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1495 CTGCCTGCCATCGGCAAGACGGAAAGGGGGAAACGCTCCACCAGGGC 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1586 A.....CCGCATCCTGCAGTACCGGGAGCTCACCAAGCTCAAG 1623
85 snGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAspVal 101
                                                                                                                                                                                                               116 oLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1674 GCTCCACACCGCTTCAACCAGAC...GGCCACGGCCAGGGCAGGCTTT 1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 ProHisSerMetSerProAlaAlaMetLeuLysSerArgGlyProVal.. 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 .....SerGlyAlaAlaMetLeu.....171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 ....ProHisHisHisHisHisHisAspMetGln...MetHisAlaAla 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 MetTyrGlyGlyThrAlaValProProProAlaGlyProProHisHisGl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 yGlyPheLeuMetProHisPro.....GlnGlySerS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1624 AACACCTACATAGACCCCCTGCCCGCCTGGTCCACCCCAAGACCGGCCG 1673
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Patent No. 5691142
GENERAL INFORMATION:
APPLICANT: Definiberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
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1035 GGGGTGCGGGGAATCCTGGC.....CAAGGACCTGGCGGTTTTGGCCC 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1126 ......GCCTACCTTCTGGACCCTCCAACACCAC 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 LeuTrpAlaMetSerArgLeu.....GlyPheAspAspTyrValGluPr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 oLeuGlyAlaTyrLeuHisArgTyrArgGluPheGluGlyAspAlaArgG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 GlyGlyAlaAsnAsnGlyGlyAlaAlaGln.GlnHisAlaAlaProAlaI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 leargGluGlnAspArgLeuMetProlleAlaAsnVallleArgIleMet 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ArgArgValLeuProAlaHisAlaLysIleSerAspAspAlaLysGluTh 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 rIleGlnGluCysValSerGluTyrIleSerPheIleThrGlyGluAlaA 85
                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,043
FILING DATE: 06 JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 26.498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-483-043-2 from: 1 to: 2496
                                 STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                     ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTOKREY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
ETLING DATE: 04-UUN-1993
APPLICATION NUMBER: US 07/986,330
                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-435-054-2 x US-08-483-043-2
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US-08-483-043-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2496 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll, Peter G.
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Percent Similarity: 45.426
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                                                                                                                                                      COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 134.50
Ratio: 0.934
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                                                                                                                                 94104
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                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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1821 CTTGGACTACAGCCAGATTGAGCTTCGGGTCCTGGCCCACCTCTCCGGGG 1870
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                                                                                                                                                                                  1401 CCA.....GCTGGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCA 1444
                                                                                                                                                                                                                                                                                                                                               1495 CTGCCTGCCATCGGCAAGACGGAGAAGACGGGGAAACGCTCCACCAGCGC 1544
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                                                                                                                                                                                                                                                          186 MetTyrGlyGlyThrAlaValProProProAlaGlyProProHisHisGl 202
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                                                                                                                                                                                                                                                                                                                    172 .... ProHisHisHisHisHisHisHisHisApMetGln... MetHisAlaAla 185
                                                              133 lyValGlyLeuValProGlyAlaAlaProSerArgGlyGlyAspHisHis 149
                                                                                                                                                                                                                                 166 .....SerGlyAlaAlaMetLeu.....171
                                                                                                                                                   150 ProHisSerMetSerProAlaAlaMetLeuLysSerArgGlyProVal.. 165
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APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: SAN FRANCISCO
STATE: CALIFORNIA
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1305 GCTTTCCCGGGTGTTGGCCCGGATGGAGGC....CACGGGGGTCCGGCTG 1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1255 CTTAAGGGAGAAAGGCCTGCTTTGGCTTTACGAGGAGGTGGAGAAGCC 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 snGluArgCysGlnArgGluGlnArgLysThrIleThrAlaGluAspVal 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 134.50 Length: 317
Ratio: 0.934 Gaps: 17
nilarity: 45.426 Percent Identity: 26.498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-481-238-2 from: 1 to: 2496
          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,238
                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER 6.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01798
TELEPHONE: (415) 705-8410
TELEFAX: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2496 base pairs
TYPE: nucleic acid
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-435-054-2 x US-08-481-238-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-481-238-2
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Percent Similarity:
                                                                                                      FILING DATE:
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185 1544	202	213 1623	215 1673	231 1720	237	249 1820	258 1870	74 919
172ProHisHisHisHisHisAspwetGlnwetHisAlaAla 185 1495 CTGCCTGCCATCGCCAAGACGGAGAAGGCGGGAAACGCTCCACCAGCGC 1544	186 MetTyrGlyGlyThralaValProProProAlaGlyProProHisHisGl :::		erhistyr	216 LeuproTyralaTyrGlubroThrTyrGlyGlyGluHisalaMetAla:	232AlaTyrTyrGlyGlyA : 1721 CCAGCTCCGAGCCTGCAGAACATCCCCGTGGGCACCCTCTGGGC	237 laAlaTyrAlaProGlyAsnGlyGlySerGlyAspGly;	250SerGlySerGlyGlyGlyGlyGlyGlyGlyGlyGl 	258 ralaSerHisThrProGlnGlySerGlyGlyLeuGluHisProHisPro 274 ::::
172	186 1545	202 1586	213 1624	216 1674	232	237 1771	250 1821	258 1871

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